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4 nucleic - nucleic search, using sw model

in on: September 24, 2004, 01:07:51; Search time 223 Seconds
(without alignments)
8291.912 Million cell updates/sec

title: US-09-964-277-20

perfect score: 3332

sequence: 1 gagagaaggagaagataata.....ataaagatgaacttggttc 3332

scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

sarched: 682709 seqs, 277475446 residues

total number of hits satisfying chosen parameters: 1365418

imum DB seq length: 0

imum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	2950	88.5	3544	4	US-09-816-494-1
2	1660	49.8	1998	4	US-09-816-494-3
3	247	7.4	279	4	US-09-016-434-91
4	225.2	6.8	2377	4	US-09-920-668-3
5	109.6	3.3	1830	4	US-09-557-921-1
6	95	2.9	2303	4	US-09-522-146-3
7	94.6	2.8	1208	4	US-09-023-655-347
8	90.2	2.7	2109	4	US-09-016-434-1135
9	90.2	2.7	2109	4	US-09-023-655-946
10	86.2	2.6	240	4	US-09-016-434-776
11	85.6	2.6	1619	4	US-09-702-705-801
12	85.6	2.6	1619	4	US-09-736-457-801
13	85.6	2.6	1619	4	US-09-614-124B-801
14	85.6	2.6	1619	4	US-09-671-325-801
15	85.6	2.6	1619	4	US-09-589-184-801
16	85.6	2.6	4337	4	US-09-702-705-804
17	85.6	2.6	4637	4	US-09-736-457-804
18	85.6	2.6	4637	4	US-09-614-124B-804
19	85.6	2.6	4637	4	US-09-671-325-804
20	85.6	2.6	4637	4	US-09-589-184-804
21	84	2.5	1238	2	US-08-530-290-11
22	84	2.5	1238	4	US-09-702-705-803
23	84	2.5	1238	4	US-09-736-457-803
24	84	2.5	1238	4	US-09-614-124B-803
25	84	2.5	1238	4	US-09-671-325-803
26	84	2.5	1238	4	US-09-589-184-803
27	84	2.5	2064	4	US-09-702-705-825

ALIGNMENTS

RESULT 1

US-09-816-494-1

; Sequence 1, Application US/09816494

; Patent No. 6664089

; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel A.

; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY

; FILE REFERENCE: 10448-030002

; CURRENT APPLICATION NUMBER: US/09/816.494

; PRIORITY FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: US 60/191,858

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3544

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (589)....(2583)

US-09-816-494-1

Query Match 88.5%; Score 2950; DB 4; Length 3544;

Best Local Similarity 95.0%; Pred. No. 0;

Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

Qy	197	GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGAGCAGAGGTAAGAATGATGTAATG	256
Db	224	GCTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGAGCAGAGGTAAGAATGATGTAATG	283
Qy	257	CGTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGTTTCCAGTCATCTCTTTATGA	316
Db	284	CGTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGTTTCCAGTCATCTCTTTATGA	343
Qy	317	ATCAAAATGTGAGGGGCTCTTTTGTGGAGCGAGTCCCTTTGCAAGAGCACATCAACGGGAAA	376
Db	344	ATCAAAATGTGAGGGGCTCTTTTGTGGAGCGAGTCCCTTTGCAAGAGCACATCAACGGGAAA	403
Qy	377	GAGAAAGAGACATTCATCTGGAGGGCTCTTGTGAAAATGGGTTTAACTCTCTTTTGGC	436
Db	404	GAGAAAGAGACATTCATCTGGAGGGCTCTTGTGAAAATGGGTTTAACTCTCTTTTGGC	463
Qy	437	AGTCACCAACCGCTGACCTCATACACATTTAGTACATGAGTGGCTGAGCTTTTGGC	496
Db	464	AGTCACCAACCGCTGACCTCATACACATTTAGTACATGAGTGGCTGAGCTTTTGGC	523
Qy	497	ACACCAACCATTCATCTGCTGGGCAAAATTAAGAGGAGGTTGGGAAAAGAGGACTTATTTG	556

2553 TCTTAACATCTGCAATTTGAGAGATCAGCTAATACTTCTCTCAACAAAATGGAAGGCGAG 2612
 2744 TCTTAACATCTGCAATTTGAGAGATCAGCTAATACTTCTCTCAACAAAATGGAAGGCGAG 2803
 2613 ATGCTAGAAATCCCTTACAG 2672
 2804 ATGCTAGAAATCCCTTACAG 2863
 2673 TGTCTTAAAAAGCAAGTGTCTTTGGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2732
 2864 TGTCTTAAAAAGCAAGTGTCTTTGGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2922
 2733 GTTGTGCTACTAAGAGATCTCAATATTAATAGTCTTTGTCCGAGCCCTTCCATAGTACACCT 2792
 2923 GTTGTGCTACTAAGAGATCTCAATATTAATAGTCTTTGTCCGAGCCCTTCCATAGTACACCT 2982
 2793 TAGCGCTCAGAGCTGAGCCAGCTTTGGGGGTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 2852
 2983 TAGCGCTCAGAGCTGAGCCAGCTTTGGGGGTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 3042
 2853 TAGTGTAAATCCCAAG 2912
 3043 TAGTGTAAATCCCAAG 3102
 2913 TGACAGCGAG 2972
 3103 TGACAGCGAG 3162
 2973 TCTACCTTAGAGCAACCCAGTACCTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3032
 3163 TCTACCTTAGAGCAACCCAGTACCTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3222
 3033 ATCTGTAGCCCATTTCTTAGGCAATGTGAATAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 3092
 3223 ATCTGTAGCCCATTTCTTAGGCAATGTGAATAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 3282
 3093 CCAATTCAAACTGTCTATGCACAAATATCCCGTGGGCTTAGATGAGAGATATTTTGT 3152
 3283 CCAATTCAAACTGTCTATGCACAAATATCCCGTGGGCTTAGATGAGAGATATTTTGT 3342
 3153 CTTCTCAGCTTTATGAAG 3212
 3343 CTTCTCAGCTTTATGAAG 3402
 3213 TGGCAACATCAGATTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCT 3272
 3403 TGGCAACATCAGATTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCT 3462
 3273 AATCAAGAGATTTGTTTAAATGCGATTTGTTTAAATGCGATTTGTTTAAATGCGATTTGTTT 3332
 3463 AATCAAGAGATTTGTTTAAATGCGATTTGTTTAAATGCGATTTGTTTAAATGCGATTTGTTT 3522

RESULT 2
 S-09-816-494-3
 Sequence 3, Application US/09816494
 Patent No. 6664089
 GENERAL INFORMATION:
 APPLICANT: Meyers, Rachel A.
 TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
 TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
 FILE REFERENCE: 10448-030002
 CURRENT APPLICATION NUMBER: US/09/816,494
 CURRENT FILING DATE: 2001-03-23
 PRIOR APPLICATION NUMBER: US 60/191,858
 PRIOR FILING DATE: 2000-03-24
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 1998
 TYPE: DNA
 ORGANISM: Homo sapiens
 S-09-816-494-3

Query Match 49.8%; Score 1660; DB 4; Length 1998;
 Best Local Similarity 91.8%; Pred. No. 0;
 Matches 1834; Conservative 0; Mismatches 0; Indels 164; Gaps 1;
 QY 562 ATGCGCCCATGAGATGATTTGGAACCTCAAAATTTGTTACTCAGAGGTTGGTCTCTCTGAA 621
 DB 1 ATGCGCCCATGAGATGATTTGGAACCTCAAAATTTGTTACTCAGAGGTTGGTCTCTCTGAA 60
 QY 622 AGTGGAAACGGAAGGCTGCTTAATTTGATAGCGGCCATTTTGGAAATACAAATACATCC 681
 DB 61 AGTGGAAACGGAAGGCTGCTTAATTTGATAGCGGCCATTTTGGAAATACAAATACATCC 120
 QY 682 CACATTTTGGAGCCATTAATATCAATGCTCCAAAGCTTATGAAGCGAGGTTGCAACAG 741
 DB 121 CACATTTTGGAGCCATTAATATCAATGCTCCAAAGCTTATGAAGCGAGGTTGCAACAG 180
 QY 742 GACAAAGTGTAAATACAGAGCTCATCCAGCAATTCAGCGAAACATTAAGTTGACATGAT 801
 DB 181 GACAAAGTGTAAATACAGAGCTCATCCAGCAATTCAGCGAAACATTAAGTTGACATGAT 240
 QY 802 TGCACTCAGAAAGGTTGATGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 861
 DB 241 TGCACTCAGAAAGGTTGATGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 300
 QY 862 GACTGTTTCTCAGTACTTCTGGTAAACTGAGAGAGCTTCAACTCTGTTTCACTG 921
 DB 301 GACTGTTTCTCAGTACTTCTGGTAAACTGAGAGAGCTTCAACTCTGTTTCACTG 360
 QY 922 CTTGC----- 926
 DB 361 CTTGAGGTTGGTGTGAGTCTCTGTTGTTTCCCTGCGCTCTGTGAAGGAAATCC 420
 QY 927 ----- 926
 DB 421 ACTCTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTTGCCAATTTGGGCAACC 480
 QY 927 -----AGAGCTGATG 937
 DB 481 CGAATTTCTCCAAATCTTTATCTTGGCTGCCAGCGAGATGTCTCAACAGAGAGCTGATG 540
 QY 938 CAGCAGATGGGATGTTGTTATGCTTAATCGCAGCATACCTGTCGAAGCCCTGACTTT 997
 DB 541 CAGCAGATGGGATGTTGTTATGCTTAATCGCAGCATACCTGTCGAAGCCCTGACTTT 600
 QY 998 ATCCCGAGTCTCATTTCTCCTGCTGCTGTGAATGACAGCTTTGTTGAGAAAATTTTG 1057
 DB 601 ATCCCGAGTCTCATTTCTCCTGCTGCTGTGAATGACAGCTTTGTTGAGAAAATTTTG 660
 QY 1058 CCGTGTGGAACAAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCCTCCAATGGATGTT 1117
 DB 661 CCGTGTGGAACAAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCCTCCAATGGATGTT 720
 QY 1118 CTAGTGCACTGTTTGTGAGGATCTCCCGCTCCCGCCACCATCGCTATCGCTTACATCATG 1177
 DB 721 CTAGTGCACTGTTTGTAGTGGGATCTCCCGCTCCCGCCACCATCGCTATCGCTTACATCATG 780
 QY 1178 AAGAGATGGACATGCTTTTGTAGTGAAGCTTACAGATTTGTGAAGAAAAGAGACTACT 1237
 DB 781 AAGAGATGGACATGCTTTTGTAGTGAAGCTTACAGATTTGTGAAGAAAAGAGACTACT 840
 QY 1238 ATATCTCCAAACTTCAATTTCTGCGCCAACTCTCGGACTATGAGAAAGAAAGTAAAGAAC 1297
 DB 841 ATATCTCCAAACTTCAATTTCTGCGCCAACTCTCGGACTATGAGAAAGAAAGTAAAGAAC 900
 QY 1298 CAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGCCAAAT 1357
 DB 901 CAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGCCAAAT 960
 QY 1358 GAACTGCTCCCTGCTGTCTCAGAGGTTGAGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1417
 DB 961 GAACTGCTCCCTGCTGTCTCAGAGGTTGAGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1020

QY 1418 TGTGCGACTCTGCTACCTCAGAGGCGAGCAGGCAAGGCGCGTGTGATCCCGCAGCGTG 1477
DB 1021 TGTGCGGACTCTGCTACCTCAGAGGCGAGCAGGCAAGGCGCGTGTGATCCCGCAGCGTG 1080
QY 1478 CCAGAGGTGCCAGCGTGAGCGCTGCTGTGTAGAGGACAGCGCGTGTGTACAGGCGCTC 1537
DB 1081 CCAGAGGTGCCAGCGTGAGCGCTGCTGTGTAGAGGACAGCGCGTGTGTACAGGCGCTC 1140
QY 1538 AGTGGGCTGCACCTGTCCGCGAGCAGGCTGGAAGACAGCAATAAGCTCAAGGCTTCCTTC 1597
DB 1141 AGTGGGCTGCACCTGTCCGCGAGCAGGCTGGAAGACAGCAATAAGCTCAAGGCTTCCTTC 1200
QY 1598 TCTCTGGATATCAAAATCAGTTTCATATTTCAGCCAGCATGGCGATGCTTCAATGCTTC 1657
DB 1201 TCTCTGGATATCAAAATCAGTTTCATATTTCAGCCAGCATGGCGATGCTTCAATGCTTC 1260
QY 1658 TCTCTCATCAGAGATGCTTTGGAAATCTACTACAACTTCCACTACTCTGGATGGGACCCAC 1717
DB 1261 TCTCTCATCAGAGATGCTTTGGAAATCTACTACAACTTCCACTACTCTGGATGGGACCCAC 1320
QY 1718 AAGCTATGCGAGTCTTCCCTGTTTCAGGAATCTATCGAGCAGACTCCCGAAACAGTCTCT 1777
DB 1321 AAGCTATGCGAGTCTTCCCTGTTTCAGGAATCTATCGAGCAGACTCCCGAAACAGTCTCT 1380
QY 1778 GATAAGGGAAGCCAGCATCCCAAGAGCTGCGAGCCGCGAGGCTTTCAGACGCCAG 1837
DB 1381 GATAAGGGAAGCCAGCATCCCAAGAGCTGCGAGCCGCGAGGCTTTCAGACGCCAG 1440
QY 1838 AGCAGCGATTGATTCGCTCAGAACCCAGCAGAGTGCGACCGCGCAGAGGTCCTTTTA 1897
DB 1441 AGCAGCGATTGATTCGCTCAGAACCCAGCAGAGTGCGACCGCGCAGAGGTCCTTTTA 1500
QY 1898 TCTCCACTGCTCAGAGTGGGAGCGTGGAGGCAATTAACACAGCAGTCTCTTTTGGC 1957
DB 1501 TCTCCACTGCTCAGAGTGGGAGCGTGGAGGCAATTAACACAGCAGTCTCTTTTGGC 1560
QY 1958 CTTTCCAGCAGCAGCAGCAGTCTCAGAACTCTGCTGGCTGGGCTTAAAGGCTGGCAG 2017
DB 1561 CTTTCCAGCAGCAGCAGCAGTCTCAGAACTCTGCTGGCTGGGCTTAAAGGCTGGCAG 1620
QY 2018 TCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGCTTTTGGC 2077
DB 1621 TCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGCTTTTGGC 1680
QY 2078 ACAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTAGCGAGGAGTCCGAGTACTCT 2137
DB 1681 ACAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTAGCGAGGAGTCCGAGTACTCT 1740
QY 2138 GCCTCAGCTGCGAGCAGCTGCTCCACTTTCGCGAGACCAAGTCTATTCTGTCGCGAGCGG 2197
DB 1741 GCCTCAGCTGCGAGCAGCTGCTCCACTTTCGCGAGACCAAGTCTATTCTGTCGCGAGCGG 1800
QY 2198 CAGAAAGCCAAAGTGCAGAGCTGACTCGCGCGCGAGCTGCGATGAAGAGAGGCCCTTTGAA 2257
DB 1801 CAGAAAGCCAAAGTGCAGAGCTGACTCGCGCGCGAGCTGCGATGAAGAGAGGCCCTTTGAA 1860
QY 2258 AAGCAGTTTAAACGAGAGAGTGCAGAAATGGAATTTGAGAGAGCATCATGTGAGAGAAC 2317
DB 1861 AAGCAGTTTAAACGAGAGAGTGCAGAAATGGAATTTGAGAGAGCATCATGTGAGAGAAC 1920
QY 2318 AGGTCAAGGAGAGCTGGGAAAGTGGGAGTCTAGCTAGCTTTTGGGCGAGCATGAA 2377
DB 1921 AGGTCAAGGAGAGCTGGGAAAGTGGGAGTCTAGCTAGCTTTTGGGCGAGCATGAA 1980
QY 2378 ATCATTTAGGCTCTCTGA 2395
DB 1981 ATCATTTAGGCTCTCTGA 1998

RESULT 3

US-09-016-434-91

; Sequence 91, Application US/09016434

; Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGFET03
CLONE: 1234795
US-09-016-434-91

Query Match 7.4%; Score 247; DB 4; Length 279;

Best Local Similarity 100.0%; Pred. No. 2e-67;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 538 GGGAAAAGAGAGACTTATTGTGTGTCATGCGCCCATGAGATGATGGAAGCTCAATTTGTTACT 597
DB 1 GGGAAAAGAGAGACTTATTGTGTGTCATGCGCCCATGAGATGATGGAAGCTCAATTTGTTACT 60
QY 598 GAGAGGTTGGTGGCTCTGCTGGAAGTGAACCGGAAAAGTGTGCTTAATTTGATAGCCGG 657
DB 61 GAGAGGTTGGTGGCTCTGCTGGAAGTGAACCGGAAAAGTGTGCTTAATTTGATAGCCGG 120
QY 658 CCATTGTGGAATACAAATACATCCCATTTTGAAGCCATTAATATCAATGCTGCTCAAG 717
DB 121 CCATTGTGGAATACAAATACATCCCATTTTGAAGCCATTAATATCAATGCTGCTCAAG 180
QY 718 CTTATGAGCGAGGTTGCAACAGGCAAAAGTGTTAATTACAGAGCTCATCCAGCATTC 777
DB 181 CTTATGAGCGAGGTTGCAACAGGCAAAAGTGTTAATTACAGAGCTCATCCAGCATTC 240
QY 778 GCGAAAC 784
DB 241 GCGAAAC 247

RESULT 4

US-09-920-668-3

; Sequence 3, Application US/09920668

; Patent No. 6482644

GENERAL INFORMATION:

APPLICANT: Lex M. Cowser
 APPLICANT: Brett P. Monia
 TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
 FILE REFERENCE: RTS-0246
 CURRENT APPLICATION NUMBER: US/09/920,668
 CURRENT FILING DATE: 2001-08-01
 NUMBER OF SEQ ID NOS: 49

SEQ ID NO 3

LENGTH: 2377

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (135)...(2012)

3-09-920-668-3

Query Match 6.8%; Score 225.2; DB 4; Length 2377;
 Best Local Similarity 60.6%; Pred. No. 7.7e-60; Mismatches 248; Indels 24; Gaps 2;
 Matches 418; Conservative 0;

927 AGGAGCTGATGACGAGATGGATGGTATGTATGTTAAATCCAGCAATACCTGTCCAA 986

|||||

670 AGGATCTGATGACGCAATATGAATGAAGTACTGTCTCAAGCCAGCAACTCTGCCCCA 729

|||||

987 AGCCTGACTTTATCCCGAGTCTCAATTCCTCGGTGCTGTGAATGACAGCTTTTGTG 1046

|||||

730 AGCTGACTTATCTCGGAGAGCGCTTCTATCGGTGCCCATCAACGACAACTACTGTG 789

|||||

1047 AGAAAAATTTGCGGTGTGGCAAAATCAGTAGATTTCATTGAGAAAGCAAGAGCTCCA 1106

|||||

790 AAAAACTGTGCGCTCGGTGCAAGTCCATCGAGTTTCATCATTAAGCAAGCTCTCCA 849

|||||

1107 ATGGATGTGTTCTAGTGCACTGTTTAGTGCGATCTCCCGCTCCGCCACCATCGTATCG 1166

|||||

850 GGTGCAAGTCACTGCTCACTGTCTGCGTGGCATCTCCCGCTCTGCCACCATCGCCATCG 909

|||||

1167 CCTACATCATGAAGAGATGAGATGTCCTTTAGATGAAGCTTTACAGATTTGTGAAGAAA 1226

|||||

910 CTTACATCATGAAGACCATGGCATGTCTCCGACGACGCTTACAGTTCTGTGAAGACA 969

|||||

1227 AAAGACCTACTATATCTCCAAATTCATTTCTGGGCCAACTCTGTGACTATGAGAAGA 1286

|||||

970 GCGCGCCGTCCTATCTCGCCCACTTCACTTCTGGCCAGCTGTGGAGTACGAGCGCA 1029

|||||

1287 AGATTGAAGAACAGACTGAGCATCAGGCCCAAGAGCAAACTCAAGCTGTGCACCTGG 1346

|||||

1030 CGCTGAAGCTGTGGCGCCCTGCGAGGGCGACCCCGGCCACCCCTCAGGGAGC---CCG 1086

|||||

1347 AGAGCCAAATGAACCTGTCCTGCTGTCTCAGAGGGTGGACAGAAAGCGAGAGCGCCC 1406

|||||

1087 AGCTCGGCCAGTCTCGCGCGCGGGGCCCGCTGCCAGCGCTGCCACCACTACTCAG 1146

|||||

1407 TCAGTCCACCTGTGCGGACTCTGTCTACCTCAGAGGCGAGCAGCAAAAGGCCCGCTGCATC 1466

|||||

1147 AGAGCGCTGCCACGACGATGGCTGCCAGGAGGGCG----- 1185

1467 CGCCAGGTGCGCCAGCTGCGCCAGCGTGGAGCGGTGTGTGTAGAGGACAGCCCGCTGG 1526

|||||

1186 GCTGAGCGCGCGGGAGCGCCCGCGCCCGCCACAGCGCCCGCGGACCGAGCGCACTGC 1245

|||||

1527 TACAGCGCTCAGTGGCTGCGACCTGTCCGACAGAGGTGGAGACAGCAATAGCTCA 1586

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1246 AGCAGGGCTGCGCGGCTGCACTCTCTCGACCGCTCTCTCGACCGCTCGAGGACACTAACCGCTCA 1305

|||||

1587 AGCGTCTCTCTCTGAGATATCAAAATCAG 1616

|||||

1306 AGCGTCTCTCTCTGAGATATCAAAATCAG 1335

|||||

8-09-557-921-1

Sequence 1, Application US/09557921

RESULT 5

8-09-557-921-1

Sequence 1, Application US/09557921

Patent No. 6551810

GENERAL INFORMATION:

APPLICANT: Lucbe, Ralf M.
 APPLICANT: Wei, Bo
 TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125.416
 CURRENT APPLICATION NUMBER: US/09/557,921
 CURRENT FILING DATE: 2000-04-20
 NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1830

TYPE: DNA

ORGANISM: Homo sapiens

US-09-557-921-1

Query Match 3.3%; Score 109.6; DB 4; Length 1830;
 Best Local Similarity 61.0%; Pred. No. 1.7e-23;
 Matches 178; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 1006 GTCTCATTTCTCGGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTGCGGTGTT 1065

|||||

Db 1187 GTTCAACTACAAAGCGGTGCCAGCTCTGACAGCAACAAAGCAGAACCTGCGGCACTT 1246

|||||

QY 1066 GGACAAATCAGTAGATTTCATTGAGAAAGCAAGCCCTCAATGGATGTGTTCTAGTGA 1125

|||||

Db 1247 TGAAGAGGCTTTTTCAGTTTCATTGAGGAAGCTCACAGTGTGGGAAGGCTTCTCATCA 1306

|||||

QY 1126 CTGTTTACTGCTGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAGAT 1185

|||||

Db 1307 CTGCAGGCTGGGTGTCCTCCGCTCCGCCACCATCGTCACTGCTTACTTGTGAGACACAC 1366

|||||

QY 1186 GGACATGCTTTTGTAGATGAAGCTTACAGATTTGTGAAAGAAAAGACCTTACTATATCTCC 1245

|||||

Db 1367 TCGGATGACCATGACTGATGCTTATAAATTTGTCAAGGCAACGACCAATATCTCCCC 1426

|||||

QY 1246 AAATTTCAATTTCTGGGCCAACTCTCGACTATGAGAAAGATTAAGAAC 1297

|||||

Db 1427 AAACCTTAATTCATGGGCGAGTTGCTAGAGTTTCGAGGAAGACCTAAACAAC 1478

|||||

RESULT 6

US-09-922-146-3

Sequence 3, Application US/09922146

Patent No. 6566133

GENERAL INFORMATION:

APPLICANT: Lex M. Cowser

APPLICANT: Brett P. Monia

TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION

FILE REFERENCE: RTS-0252

CURRENT APPLICATION NUMBER: US/09/922,146

CURRENT FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 48

SEQ ID NO 3

LENGTH: 2303

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (114)...(1268)

US-09-922-146-3

Query Match 2.9%; Score 95; DB 4; Length 2303;
 Best Local Similarity 58.8%; Pred. No. 8.1e-19;
 Matches 164; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 1004 GAGTCTCATTTCTCGGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCTGG 1063

|||||

Db 858 GACTTTCATCAAGCAGATCCCATCTCCGACCACTGGAGCCAGAACCTGTGCGGTTC 917

|||||

QY 1064 TTGGACAAATCAGTAGATTTCATTGAGAAAGCAAGCCCTCAATGGATGTGTTCTAGTG 1123

|||||

Db 918 TTTCGAGGAGCCATTGAGTTCAATGATGAGGCTTGTCCAGAACTGCGGGGTCTGCTGTC 977

|||||

	1124	CACGTGTTAGCTGGATCTCCCGCTCCGCCAACAATCGCTCATCATGAAGAGG	1183
Oy			
	978	CACGTCTGGCGGGGTCA GCGGTTCTGTCAACCGTCACTGTGGCCTACCTCATGCAGAAG	1037
Db			
	1184	ATGGACATGTCCTTAGATGAAGCTTACAGATTGTTGGAAAGAAAAGAACCTACTATATCT	1243
Oy			
	1038	CTCACCTCTCTCAACGATGCCTATGACCTGGTCAAGAGGAAGAGTCTAACATCTCC	1097
Db			
	1244	CCAACTTCAATTTCTGGGCGCACTCCTGGACTATGAG	1282
Oy			
	1098	CCCAACTTCAACTTTCATGGGCGCAGTGCTGGACTTTGAG	1136
Db			

RESULT 7
US-09-023-655-347
; Sequence 347, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: COCKS, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

Query Match	2.8%	Score 94.6	DB 4	Length 1208
Best Local Similarity	64.3%	Pred. No. 6.6e-19		
Matches 142	Conservative	0	Mismatches 79	Indels 0
				Gaps 0

1137 GGATCTCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGGATGGACATGCTT 1196

64	GGGTGTCCCGCTCGCCACCATCGTCATCGCTTACTTGATGAAGCACACTCGGATGACCA	123
1197	TAGATGAGGCTTACAGATTTGTGAAGAAAAAGACCTACTATATCTCCAAACTTCAATT	1256
124	TGACTGATGCTTTATAAATTTGTCAAGGCGAAGCGACCAATATATCTCCCCAAACCTTAAC	183
1257	TTCTGGGGCCAACTCCTCGCATATGAGAAGAGATTAAGAAC	1297
184	TCATGGGGCAGTTGCTAGAGTTTCGAGGAAGACCTAAACAAC	224

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	Query Match	2.7%;	Score 90.2;	DB 4;	Length 2109;
	Best Local Similarity	57.1%;	Pred. No. 2.5e-17;		
	Matches 164;	Conservative	0;	Mismatches 123;	Indels 0;
	Gaps	0;			
QY	1004	GAGTCTCATTTCTCGCTGTGCTGTGAATGACAGCTTTTGTGAGAAAAATTTTGCCTGG	1063		
DB	1105	GAGTTTAAATACAGCAAAATCCCATCTCGGATCACTGGAGCCAAAACCTGTGCCAGTTT	1164		
QY	1064	TTGAGCAAAATCAGTAGATTTTCATTTGAGAAGCAAAAGCCCTCAATGGATGTGTTCTAGTG	1123		
DB	1165	TTCCCTTGAGGCCATTTCTTTTCATAGATGAAGCCGGGCAAGAACTGTGGTGCTCTGGTA	1224		
QY	1124	CACTGTTTACGTGGGATCTCCCGCTCCGCCACCATCGCTTATCGCCTACATCATGAAGAGG	1183		

1225 CATTGCTTGGCTGGCATTAGCGGCTCAGTCACTGTGACTGTGGCTTACCTTATGCGAGAAG 1284
1184 ATGGACATGCTTTAGATGAAGCTTACAGATTGTGGAAGAAAAAGACCTACTATATCT 1243
1285 CTCAATCTGTGATGAAGCATGCTTATGACATGTGCAAAATGAAAAATCCACATATCC 1344
1244 CCAAACTTCAATTTTCTGGGCAACTCCTGGCACTATGAGAAGAGAT 1290
1345 CCTAACTTCAACTTCAATGGTTCAGTGTGGACTTCGAGAGAGCGCT 1391

RESULT 9
3-09-023-655-946
Sequence 946, Application US/09023655
Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 946:
SEQUENCE CHARACTERISTICS:
LENGTH: 2103 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENEBANK
CLONE: g1418933

S-09-023-655-946

Query Match 2.7%; Score 90.2; DB 4; Length 2109;
Best Local Similarity 57.1%; Pred. No. 2.5e-17;
Matches 164; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Y 1004 GAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTGGCGTGG 1063
b 1105 GAGTTTAAATACAAGCAAAATCCCATCTCGGATCACTGGAGCCAAAACCTGTCCCACTTT 1164
Y 1064 TTGGCAAAATCAGTAGATTTTCATTGTGAGAAAGCAAAAGCCCTCCCAATGATGTTCTTAGTG 1123
b 1165 TTCCCTCAGGCCAATTTCTTTTCATAGATGAAGCCGGGCAAGAACTGTGTGTCCTTGGTA 1224
Y 1124 CACTGTTTAGTGGGATCTCCCGCTCCGCCAATCGCTATCGCTTACATCATGAAGAGG 1183

Db 1225 CATTGCTTGGCTGGCATTAGCGGCTCAGTCACTGTGACTGTGGCTTACCTTATGCGAGAAG 1284
QY 1184 ATGGACATGCTTTAGATGAAGCTTACAGATTGTGGAAGAAAAAGACCTACTATATCT 1243
Db 1285 CTCAATCTGTGATGAAGCATGCTTATGACATGTGCAAAATGAAAAATCCACATATCC 1344
QY 1244 CCAAACTTCAATTTTCTGGGCAACTCCTGGCACTATGAGAAGAGAT 1290
Db 1345 CCTAACTTCAACTTCAATGGTTCAGTGTGGACTTCGAGAGAGCGCT 1391

RESULT 10
US-09-016-434-776
Sequence 776, Application US/09016434
Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 776:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LIVRBCT01
CLONE: 480457

US-09-016-434-776
Query Match 2.6%; Score 86.2; DB 4; Length 240;
Best Local Similarity 66.5%; Pred. No. 8.5e-17;
Matches 121; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1116 TTCTAGTGCACGTGTTAGTGGGATCTCCGCTCCGCCACCATCGCTATCGCTACATCA 1175
Db 10 TTCTCATCCATCCGCGGCTGGGGTGTCCCGTCCGNCACCATCGCTATCGTTACTTGA 69
QY 1176 TGAAGAGGATGACATGTCTTTAGATGAAGCTTTACAGATTTGTGAAAGAAAAAGACCTA 1235
Db 70 TGAGACACANTCGGATGACCATGACTGCTTATAATTTGTCAAAGGCAACGACCAA 129
QY 1236 CTATATCTCCAAACTTCAATTTTGTGGGCCAACTCTGTGAGATATGAGAAAGATTAAAGA 1295

Db 130 TTATCTNCCAAACCTTAACCTTCATGGGGCAGTTGCTAGAGTTTCGAGGAGACCTAAACA 189
QY 1296 AC 1297
Db 190 AC 191

RESULT 11

US-09-702-705-801

; Sequence 801, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 801

; LENGTH: 1619

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-702-705-801

Query Match 2.6%; Score 85.6; DB 4; Length 1619;
Best Local Similarity 53.6%; Pred. No. 5.7e-16;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 993 ACTTTATCCCGAGTCTCATTTCTCGGTGTCGCTGTAATGACAGCTTTTGTGAGAAA 1052

Db 429 ACTTTGAAGGACATCATAGTCAAGTGCATCCAGTGGAGATAACCAAGGCCGACA 488

QY 1053 TTTTGGCCGTGTTGGACAAATCAGTAGATTTTATTGAGAAAGCAAAAGCCTCCATGGAT 1112

Db 489 TCAGTCTCTGGTTCATGGAAGCCATAGATACATCGATGCCGTGAAGGACTGCCGTGGC 548

QY 1113 GTGTTCTAGTGCACCTGTTTGTAGTGGATCTCCCGTCCGCCACCATCGCTATCGCTACA 1172

Db 549 GCGTGTGTGTGCTGCTGCGAGCGGCACTCCGGTGGCCACCATCTGCTGGCCTACC 608

QY 1173 TCATGAAGAGGATGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAGAC 1232

Db 609 TGATGATGAAGAAACGGGTGAGGCTGAGGAGCCTTCGAGTTCTTAAGCAGCCCGCA 668

QY 1233 CTACTATATCTCCAACTTCAATTTTCTGGGCCAACTCTCTGGACTATGAGAAGAGATTA 1292

Db 669 GCATTATCTCGCCCACTTTCAGCTTCATGGGGCAGCTGTGCAAGTTCGAGTCCCAAGTGC 728

QY 1293 AGAACCACTGAGCATCAGGCCCAAGAGC 1324

Db 729 TGGCCAGCTCTGTGCTGGAGGCTGTAGC 760

RESULT 12

US-09-736-457-801

; Sequence 801, Application US/09736457

; Patent No. 6509448

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

QY 1173 TCATGAAGAGATGGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAGAAAAAGAC 1232
Db 609 TGATGATGAAGAACGGGTGAGGCTTGAGGAGGCTTCGAGTTCTTAAAGAGCCCGCA 668
QY 1233 CTACTATATCTCCAAACTTCAATTTCTTGGGCCAACTCTCTGACTATGAGAAGATT 1292
Db 669 GCATTATCTGCCCAACTTCAGCTTCATGCGGAGCTGCTGCAGTTCGAGTCCAGGTGC 728
QY 1293 AGAACAGAGATGGAGCATCAGGGCCAAAGAGC 1324
Db 729 TGGCCAGCTCTGTGCTGCGGAGGCTGCTAGC 760

RESULT 15
US-09-589-184-801
; Sequence 801, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-589-184-801

Query Match 2.6%; Score 85.6; DB 4; Length 1619;
Best Local Similarity 53.6%; Pred. No. 5.7e-16;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
QY 993 ACTTTATCCCGAGTCTCATTTCTCGCTGTGCTGTAATGACAGCTTTTGTGAGAAAA 1052
Db 429 ACTTTGAAGGACACTATACAGTACAGTCCATCCAGTGGAGATTAACCAAGGCCGACA 488
QY 1053 TTTTGCCTGTGTGGACAAATCAGTAGATTTTCATTGAGAAAGCAAGCCTCCAATGGAT 1112
Db 489 TCAGCTCCTGTTCATGGAAGCCATAGAGTACATCATGCGGTGAAGGACTGCGCTGGGC 548
QY 1113 GTGTTCTAGTGCACCTGTTTAGTGGATCTCCCGTCCGCCACCATCGCTATCGCTACA 1172
Db 549 GCGTGTGCTGCACTGCCAGCGGCGCATCTCGCGTCCGCCACCATCTGCGCTGGCTACC 608
QY 1173 TCATGAAGAGATGGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAGAAAAAGAC 1232
Db 609 TGATGATGAAGAACGGGTGAGGCTTGAGGAGGCTTCGAGTTCTTAAAGAGCCCGCA 668
QY 1233 CTACTATATCTCCAAACTTCAATTTCTTGGGCCAACTCTCTGACTATGAGAAGATT 1292
Db 669 GCATTATCTGCCCAACTTCAGCTTCATGCGGAGCTGCTGCAGTTCGAGTCCAGGTGC 728
QY 1293 AGAACAGAGATGGAGCATCAGGGCCAAAGAGC 1324
Db 729 TGGCCAGCTCTGTGCTGCGGAGGCTGCTAGC 760

Search completed: September 24, 2004, 02:12:58
Job time : 232 secs

Query Match 2.6%; Score 85.6; DB 4; Length 1619;
Best Local Similarity 53.6%; Pred. No. 5.7e-16;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
QY 993 ACTTTATCCCGAGTCTCATTTCTCGCTGTGCTGTAATGACAGCTTTTGTGAGAAAA 1052
Db 429 ACTTTGAAGGACACTATACAGTACAGTCCATCCAGTGGAGATTAACCAAGGCCGACA 488
QY 1053 TTTTGCCTGTGTGGACAAATCAGTAGATTTTCATTGAGAAAGCAAGCCTCCAATGGAT 1112
Db 489 TCAGCTCCTGTTCATGGAAGCCATAGATACATCATGATGCCGTGAAGACTGCGCTGGGC 548
QY 1113 GTGTTCTAGTGCACCTGTTTAGTGGATCTCCCGTCCGCCACCATCGTATCGCTACA 1172
Db 549 GCGTGTGCTGCACTGCCAGGCGGCATCTCGCGTCCGCCACCATCTGCGCTGGCTACC 608
QY 1173 TCATGAAGAGATGGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAGAAAAAGAC 1232
Db 609 TGATGATGAAGAACGGGTGAGGCTTGAGGAGGCTTCGAGTTCTTAAAGAGCCCGCA 668
QY 1233 CTACTATATCTCCAAACTTCAATTTCTTGGGCCAACTCTCTGACTATGAGAAGATT 1292
Db 669 GCATTATCTGCCCAACTTCAGCTTCATGCGGAGCTGCTGCAGTTCGAGTCCAGGTGC 728
QY 1293 AGAACAGAGATGGAGCATCAGGGCCAAAGAGC 1324
Db 729 TGGCCAGCTCTGTGCTGCGGAGGCTGCTAGC 760

RESULT 14
3-09-671-325-801
; Sequence 801, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Lique
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
3-09-671-325-801

Query Match 2.6%; Score 85.6; DB 4; Length 1619;
Best Local Similarity 53.6%; Pred. No. 5.7e-16;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
QY 993 ACTTTATCCCGAGTCTCATTTCTCGCTGTGCTGTAATGACAGCTTTTGTGAGAAAA 1052
Db 429 ACTTTGAAGGACACTATACAGTACAGTCCATCCAGTGGAGATTAACCAAGGCCGACA 488
QY 1053 TTTTGCCTGTGTGGACAAATCAGTAGATTTTCATTGAGAAAGCAAGCCTCCAATGGAT 1112
Db 489 TCAGCTCCTGTTCATGGAAGCCATAGATACATCATGATGCCGTGAAGACTGCGCTGGGC 548
QY 1113 GTGTTCTAGTGCACCTGTTTAGTGGATCTCCCGTCCGCCACCATCGTATCGCTACA 1172
Db 549 GCGTGTGCTGCACTGCCAGGCGGCATCTCGCGTCCGCCACCATCTGCGCTGGCTACC 608

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Db	181	GTCCGGCCGCCAAAGAGCTTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGAGCAAGGT	240
Qy	241	AAAGAAATGATGTAATGGCGTGGCTGCTCAAGAGCATCTTTTGTGTTGGAAATGGTTATTC	300
Db	241	AAAGAAATGATGTAATGGCGTGGCTGCTCAAGAGCATCTTTTGTGTTGGAAATGGTTATTC	300
Qy	301	AGTCATCTCTTTATGAAATCAAAATGAGGGGCTGTTGTCAGCGAGTCCCTTTTGAAGA	360
Db	301	AGTCATCTCTTTATGAAATCAAAATGAGGGGCTGTTTGTGACGAGTCCCTTTTGAAGA	360
Qy	361	GCACATCAACGGGAAGAGAGAGACATTCATCTGGAGGGCTCTTGTGAAATGGGTT	420
Db	361	GCACATCAACGGGAAGAGAGAGACATTCATCTGGAGGGCTCTTGTGAAATGGGTT	420
Qy	421	TAACTCTCTCTTTTGGCAGTCACCAAGCGCTGACCTCATACATCTTTTATGTAACAATGGAGT	480
Db	421	TAACTCTCTCTTTTGGCAGTCACCAAGCGCTGACCTCATACATCTTTTATGTAACAATGGAGT	480
Qy	481	GGCTGAGCTTTTGAGCACACCAACCATTAATCATCTGTGGCAAAATTAAGAGAGAGTGGG	540
Db	481	GGCTGAGCTTTTGAGCACACCAACCATTAATCATCTGTGGCAAAATTAAGAGAGAGTGGG	540
Qy	541	AAAGAGGACTTATCTGTCATGCGCCCATGAGATGATTGGAACCTCAAAATCTTACTGAG	600
Db	541	AAAGAGGACTTATCTGTCATGCGCCCATGAGATGATTGGAACCTCAAAATCTTACTGAG	600
Qy	601	AGTTTGGTGGCTCTGCTGGAAGAGTGGAAACGGAAGAGTCTCTAAATGATAGCGGCCA	660
Db	601	AGTTTGGTGGCTCTGCTGGAAGAGTGGAAACGGAAGAGTCTCTAAATGATAGCGGCCA	660
Qy	661	TTTGTGGAATACAATACATCCCAATTTTGGAGGCATTAATACATCAATCTGCTCCAGCTT	720
Db	661	TTTGTGGAATACAATACATCCCAATTTTGGAGGCATTAATACATCAATCTGCTCCAGCTT	720
Qy	721	ATGAGCGAAGTGGCAACAGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCG	780
Db	721	ATGAGCGAAGTGGCAACAGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCG	780
Qy	781	AAACATAAGTTGACATTCATTCAGTCAAGAGTGTAGTTTACGATCAAAAGCTCCCAA	840
Db	781	AAACATAAGTTGACATTCATTCAGTCAAGAGTGTAGTTTACGATCAAAAGCTCCCAA	840
Qy	841	GATGTTGCTCTCTCTTCAGACTGTTTCTCACTGTACTTCTGGGTAAACTGGAGAG	900
Db	841	GATGTTGCTCTCTCTTCAGACTGTTTCTCACTGTACTTCTGGGTAAACTGGAGAG	900
Qy	901	AGCTTCAACTCTGTTCACTGTTGAGAGCTGATGACAGCAATGGGATTTGTTATGT	960
Db	901	AGCTTCAACTCTGTTCACTGTTGAGAGCTGATGACAGCAATGGGATTTGTTATGT	960
Qy	961	GTTAAATGCCAGCAATACCTGTCGAAGCTGATTTATCCCGAGTCTCATTTCTCTGG	1020
Db	961	GTTAAATGCCAGCAATACCTGTCGAAGCTGATTTATCCCGAGTCTCATTTCTCTGG	1020
Qy	1021	TGTGCTGTGAATGACAGCTTTTGTGAGAAATTTTGGCGTGGTGGCAAAATCAGTAGA	1080
Db	1021	TGTGCTGTGAATGACAGCTTTTGTGAGAAATTTTGGCGTGGTGGCAAAATCAGTAGA	1080
Qy	1081	TTTCAATTGAGAAAGCAAAAGCTTCAATGATGTTGTTTCTAGTGCATGTTTGGGAT	1140
Db	1081	TTTCAATTGAGAAAGCAAAAGCTTCAATGATGTTGTTTCTAGTGCATGTTTGGGAT	1140
Qy	1141	CTCCCGCTCGCCACCATCTGCTATCGCTTACATCATGAGAGATGGAATCTCTTTTGA	1200
Db	1141	CTCCCGCTCGCCACCATCTGCTATCGCTTACATCATGAGAGATGGAATCTCTTTTGA	1200
Qy	1201	TGAAGCTTACAGATTTGTGAGAAAGAAAGACCTACTATATCTCCAAATCTTCAATTTCT	1260
Db	1201	TGAAGCTTACAGATTTGTGAGAAAGAAAGACCTACTATATCTCCAAATCTTCAATTTCT	1260
Qy	1261	GGGCCAACTCTCTGGAATGAGAGAGATTAAGAACCAAGCTGAGCATCAGGGCCAAA	1320
Db	1261	GGGCCAACTCTCTGGAATGAGAGAGATTAAGAACCAAGCTGAGCATCAGGGCCAAA	1320
Qy	1321	GAGCAAACTCAAGCTGTGCACTGGAGAGCCAAATGAACCTGTCTCTGTCTCTCAGA	1380
Db	1321	GAGCAAACTCAAGCTGTGCACTGGAGAGCCAAATGAACCTGTCTCTGTCTCTCAGA	1380
Qy	1381	GGTGGACAGAAAAGCAGAGCGCCCTCAGTCCACCTGTGCGGACTCTCTCTCTCAGA	1440
Db	1381	GGTGGACAGAAAAGCAGAGCGCCCTCAGTCCACCTGTGCGGACTCTCTCTCTCAGA	1440
Qy	1441	GGCAGCGGACAAAGGGCCCGTGATCCCGCAGCGTCCAGCGCTGCGGAGCC	1500
Db	1441	GGCAGCGGACAAAGGGCCCGTGATCCCGCAGCGTCCAGCGCTGCGGAGCC	1500
Qy	1501	GTCCCTGTAGAGGACAGCGCGCTGATCAGGGGCTCAAGTGGGCTGCACCTGTCGCGAGA	1560
Db	1501	GTCCCTGTAGAGGACAGCGCGCTGATCAGGGGCTCAAGTGGGCTGCACCTGTCGCGAGA	1560
Qy	1561	CAGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTCTCTCTGGATATCAAAATCAGTTTC	1620
Db	1561	CAGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTCTCTCTGGATATCAAAATCAGTTTC	1620
Qy	1621	ATATTGAGCCAGTATGAGCATCTCTTACATGAGTTCCTCTCTCATCAAGATGCTTTGGA	1680
Db	1621	ATATTGAGCCAGTATGAGCATCTCTTACATGAGTTCCTCTCTCATCAAGATGCTTTGGA	1680
Qy	1681	ATACTCAAACTTCCACTACTCTGGATGGGACCAACAGCTATGCGGCTTCTCCCTGT	1740
Db	1681	ATACTCAAACTTCCACTACTCTGGATGGGACCAACAGCTATGCGGCTTCTCCCTGT	1740
Qy	1741	TCAGAACTATCGGAGCAGACTCCGGAACAGCTCTGATAGGAGCAAGCAGCATCCC	1800
Db	1741	TCAGAACTATCGGAGCAGACTCCGGAACAGCTCTGATAGGAGCAAGCAGCATCCC	1800
Qy	1801	CAAGAACTGACAGACCGCCAGGCTTCAGACAGCAGCAGCAAGCATTCGGTTCAG	1860
Db	1801	CAAGAACTGACAGACCGCCAGGCTTCAGACAGCAGCAGCAAGCATTCGGTTCAG	1860
Qy	1861	AACAGCAGCAGTGGGCGCCAGAGTCTCTTTTATCTCTCACTGATCGAAGTGGAG	1920
Db	1861	AACAGCAGCAGTGGGCGCCAGAGTCTCTTTTATCTCTCACTGATCGAAGTGGAG	1920
Qy	1921	CGTGGAGCAATTTACCAACAGCTTCTTTTGGGCTTTCACAGCAGCAGCAGCATCT	1980
Db	1921	CGTGGAGCAATTTACCAACAGCTTCTTTTGGGCTTTCACAGCAGCAGCAGCATCT	1980
Qy	1981	CACGAAGTCTCGGCTTGGGCTTAAAGGCTGGCACTCGGATATCTTGGCCCCCAGAC	2040
Db	1981	CACGAAGTCTCGGCTTGGGCTTAAAGGCTGGCACTCGGATATCTTGGCCCCCAGAC	2040
Qy	2041	CTCTACCCCTTCCCTGACACAGCTGATTTTGGCAAGAGTCTCTCACTCTACTC	2100
Db	2041	CTCTACCCCTTCCCTGACACAGCTGATTTTGGCAAGAGTCTCTCACTCTACTC	2100
Qy	2101	TGCTCTAGCCATCTACGGAGCAGTCCAGTACTCTGCTTACAGCTGCGAGCTGCC	2160
Db	2101	TGCTCTAGCCATCTACGGAGCAGTCCAGTACTCTGCTTACAGCTGCGAGCTGCC	2160
Qy	2161	CACTTGCGGAGCAAGTCTATTCTGTGCGCAGCGGCGAGGCAAGTGCAGAGCTGA	2220
Db	2161	CACTTGCGGAGCAAGTCTATTCTGTGCGCAGCGGCGAGGCAAGTGCAGAGCTGA	2220
Qy	2221	CTCGCGGAGCTGGCATGAAGAGAGCCCTTTTGAAGAGCAGTTTAAACGCAAGCTG	2280
Db	2221	CTCGCGGAGCTGGCATGAAGAGAGCCCTTTTGAAGAGCAGTTTAAACGCAAGCTG	2280
Qy	2281	CCAAATGGAATTTGGAGAGAGCATGATCAGAGAAAGGTCACGGGAGAGCTGGGAA	2340
Db	2281	CCAAATGGAATTTGGAGAGAGCATGATCAGAGAAAGGTCACGGGAGAGCTGGGAA	2340
Qy	2341	AGTGGGAGCTCAGCTAGCTTTTGGGAGCAGCATGGAATCATTCAGGCTCTCTCAGAAGA	2400
Db	2341	AGTGGGAGCTCAGCTAGCTTTTGGGAGCAGCATGGAATCATTCAGGCTCTCTCAGAAGA	2400

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; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

Query Match      94.8%; Score 3158; DB 9; Length 3496;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 3332; Conservative 0; Mismatches 0; Indels 164; Gaps 1;

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61  GCGAGCGGAGCGAGCGCGCCCTCTCGGCTCCGCGCGCGCGCTCGCAAGTCGCGAGGC 120
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121  GAGGGGGCCCGAGGGGAGAGCCCGTGAACAATTCCTTCCTCTGAGGGAATTCGGAG 180
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121  GAGGGGGCCCGAGGGGAGAGCCCGTGAACAATTCCTTCCTCTGAGGGAATTCGGAG 180
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181  GTCGCGCGGCCCCMAAGCTTTTCAGTCCAGTGTAAAGCTCTTGAGCGCGGGAGCAAGGT 240
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181  GTCGCGCGGCCCCMAAGCTTTTCAGTCCAGTGTAAAGCTCTTGAGCGCGGGAGCAAGGT 240
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241  AAAGAAATGATGTAAATGCGCTGGCTCTCCAAAGCATCTTTGTTGGAAATGTTATTC 300
   |||
241  AAAGAAATGATGTAAATGCGCTGGCTCTCCAAAGCATCTTTGTTGGAAATGTTATTC 300
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301  AGTCATCTCTTTATGAATCAAAATGTGAGGGGTGCTTTGTGACGGAGTCTCTTGCAAGA 360
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301  AGTCATCTCTTTATGAATCAAAATGTGAGGGGTGCTTTGTGACGGAGTCTCTTGCAAGA 360
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361  GCACATCAACGCGAAAGAGAGAGACATTCACCTTGAGGGGTCTTGCTGAAATGGGTT 420
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361  GCACATCAACGCGAAAGAGAGAGACATTCACCTTGAGGGGTCTTGCTGAAATGGGTT 420
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421  TAACTCTCTCTTTGCGAGTCACACCGAGCTGACCTCATACACTTTTAGTACAAATGGAGT 480
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421  TAACTCTCTCTTTGCGAGTCACACCGAGCTGACCTCATACACTTTTAGTACAAATGGAGT 480
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481  GCGTGAGCCTTTGAGCACAACCAATTCATCATCGTGGCAAAATTAAGAGAGAGGTGGG 540
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481  GCGTGAGCCTTTGAGCACAACCAATTCATCATCGTGGCAAAATTAAGAGAGAGGTGGG 540
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541  AAAAGAGACATTAATGTTGTGATGCGCCATCGAGATCATTTGGAACTCAAAATGTTACTGAG 600
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541  AAAAGAGACATTAATGTTGTGATGCGCCATCGAGATCATTTGGAACTCAAAATGTTACTGAG 600
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601  AGTTGTGTGGCTCTGCTGGAAGTGGAAAGGAAAGTCTGCTTAATGATAGCCGGCCCA 660
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601  AGTTGTGTGGCTCTGCTGGAAGTGGAAAGGAAAGTCTGCTTAATGATAGCCGGCCCA 660
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661  TTTGTGGAATACAATPACATCCCAATTTTGAAGCGCAATTAATACAACTGCTCCAAAGCTT 720
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721  ATGAGCGCAAGGTTCGACACGAGACAAGGTGTAATTTACAGAGCTCATCCAGCAATTCAGCG 780
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721  ATGAGCGCAAGGTTCGACACGAGACAAGGTGTAATTTACAGAGCTCATCCAGCAATTCAGCG 780
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781  AAACATAAGGTTGCAATTTGATGTCAGTCAGAAAGGTTGTAGTTTACGATCAAAAGCTCCCAA 840
   |||
781  AAACATAAGGTTGCAATTTGATGTCAGTCAGAAAGGTTGTAGTTTACGATCAAAAGCTCCCAA 840
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841  GATGTTGCTCTCTCTCTTCAGACTGTTTCTCAGTGTACTTCTGCGGTAAACTGGAGAAG 900
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TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE

2897	CAAAACCAACGCTCACTGTGACACGCGAGGGGACACGAGCATCACTCTGCTGACCGGACCCATT	29556
3061	CAAAACCAACGCTCACTGTGACACGCGAGGGGACACGAGCATCACTCTGCTGACCGGACCCATT	3120
2957	AGGGGCCCTTGGCAAGAGTCTACCTTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTCCGGG	3016
3121	AGGGGCCCTTGGCAAGAGTCTACCTTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTCCGGG	3180
3017	CTTTGACCACTACCATATCTGGTAGGCCATTTTCTTAGGCCAATTTGTGAATAGGTAGGTAGCT	3076
3181	CTTTGACCACTACCATATCTGGTAGGCCATTTTCTTAGGCCAATTTGTGAATAGGTAGGTAGCT	3240
3077	AGTCACACTTTTTCAGACCAATTCAAACTGTCTATGACACAAATTCCTGTGGGCGCTAGATG	3136
3241	AGTCACACTTTTTCAGACCAATTCAAACTGTCTATGACACAAATTCCTGTGGGCGCTAGATG	3300
3137	GAGATAATTTTTTTTCTCTCTCAGCTTTATGAAGAGAGGAAACTGTCTAGGATTCAGC	3196
3301	GAGATAATTTTTTTTCTCTCTCAGCTTTATGAAGAGAGGAAACTGTCTAGGATTCAGC	3360
3197	TGAACCCACAGAACCTGGCAACATCAGATTTAAGCTTAAGCTTGGAGCTTAACGAGTC	3256
3361	TGAACCCACAGAACCTGGCAACATCAGATTTAAGCTTAAGCTTGGAGCTTAACGAGTC	3420
3257	TACCTCCCTCTTTGTAATCAAGAAATGTTTAAATGGGATTTGTCAATCCTTTAAATAA	3316
3421	TACCTCCCTCTTTGTAATCAAGAAATGTTTAAATGGGATTTGTCAATCCTTTAAATAA	3480
3317	AGATGAACCTTGGTTTC	3332
3481	AGATGAACCTTGGTTTC	3496

RESULT 3
 -10-425-114-26234
 Sequence 26234, Application US/10425114
 Publication No. US20040034888A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

APPLICANT: CAO, JONGWEI
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53313) B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 26234
 LENGTH: 3625
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
 S-10-425-114-26234

Query Match	94.4%	Score 3145;	DB 13;	Length 3625;
Best Local Similarity	95.3%;	0; Mismatches	0; Indels 165;	Gaps 2;
Matches 3330;	Conservative			
2	AGAGAGGAGGAGAGTAATATCTGAAAGAGAGAGGAGGAGGAGCCACGGGACGGGACG	61		
132	AGAGAGGAGGAGAGTAATATCTGAAAGAGAGAGGAGGAGGAGCCACGGGACGGGACG	191		
62	CGAGCGGAGGCGAGCGGCCCTCTCGGCTCCGCGCGCGCGCCTCGCAAGTCCCGGAGGCG	121		
192	CGAGCGGAGGCGAGCGGCCCTCTCGGCTCCGCGCGCGCGCCTCGCAAGTCCCGGAGGCG	251		
132	AGGGGGGCGGAGGGGAGACGCGGTGACAACTTTCGTTTCCCTCTGAGGGAATTCGGAGG	181		
252	AGGGGGGCGGAGGGGAGACGCGGTGACAACTTTCGTTTCCCTCTGAGGGAATTCGGAGG	311		

QY	1098	AAGCCTCCAAATGGATGTTCTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGCCACCA	1157	DB	2472	TCTATTCTGTGCGCAGCGCGCAGAAAGCCAGTGCAGAGCTGACTCGCGCGGAGCTGGC	2531
DB	1392	AAGCCTCCAAATGGATGTTCTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGCCACCA	1451	QY	2238	ATGAAGAGAGCCCTTTTGAAGCAGTTTAAACGACAGCTGCAAAATGGAATTTGGAG	2297
QY	1158	TGCTATCGCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTGG	1217	DB	2532	ATGAAGAGAGCCCTTTTGAAGCAGTTTAAACGACAGCTGCAAAATGGAATTTGGAG	2591
DB	1452	TGCTATCGCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTGG	1511	QY	2298	AGACATCATGTTCAGAGAACAGGTTCACGGGAGAGCTGGGGAAGTGGGAGTCACTCA	2357
QY	1218	TGAAGAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCTGGACT	1277	DB	2592	AGACATCATGTTCAGAGAACAGGTTCACGGGAGAGCTGGGGAAGTGGGAGTCACTCA	2651
DB	1512	TGAAGAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCTGGACT	1571	QY	2358	GCTTTTGGGCGAGCATGGAATCATTCAGGTCTCTCAGAGGAAGACACTTTGTGACTTC	2417
QY	1278	ATGAGAGAGATTAAGAACACAGCTGGAGCATCAGGCGCAAGAGCAACTCAAGCTGC	1337	DB	2652	GCTTTTGGGCGAGCATGGAATCATTCAGGTCTCTCAGAGGAAGACACTTTGTGACTTC	2711
DB	1572	ATGAGAGAGATTAAGAACACAGCTGGAGCATCAGGCGCAAGAGCAACTCAAGCTGC	1631	QY	2418	TATAGACAAATTTTTTTTCTTTGTTTCACAAAAAATTCCTGTAAATCTGAAATATATA	2477
QY	1338	TGCACCTGGAGAGCCAAATGAACCTGTCTCTGCTGTCTCAGAGGTGGACAGAAAAGCG	1397	DB	2712	TATAGACAAATTTTTTTTCTTTGTTTCACAAAAAATTCCTGTAAATCTGAAATATATA	2771
DB	1632	TGCACCTGGAGAGCCAAATGAACCTGTCTCTGCTGTCTCAGAGGTGGACAGAAAAGCG	1691	QY	2478	TGTACATACATATATATTTTTTGGAAATGGAGCTATGTTGTAAAGCAACAGGTGATCA	2537
QY	1398	AGACGCCCTCAGTCCACCTGTGCGGACTCTGTACTCTCAGAGGACAGGACAAAGGC	1457	DB	2772	TGTACATACATATATATTTTTTGGAAATGGAGCTATGTTGTAAAGCAACAGGTGATCA	2831
DB	1692	AGACGCCCTCAGTCCACCTGTGCGGACTCTGTACTCTCAGAGGACAGGACAAAGGC	1751	QY	2538	ACCCAGTTGTACTCTCTTAACATCTGCATTTGAGAGATCAGCTAACTTCTCTCAACA	2597
QY	1458	CCGTGATCCCGCAGCGTGCCAGGCTGCCAGGTCGCCAGGTCGCTGTGTAGAGGACA	1517	DB	2832	ACCCAGTTGTACTCTCTTAACATCTGCATTTGAGAGATCAGCTAACTTCTCTCAACA	2891
DB	1752	CCGTGATCCCGCAGCGTGCCAGGTCGCCAGGTCGCTGTGTAGAGGACA	1811	QY	2598	AAAAAGGAGGACAGTGTAGAAATCCCTCAGAGGAGGAAAAACCATTTTATTCAGTG	2657
QY	1518	GCCCGTGATCAGAGGCTCAGTGCGGCTGCACCTGTCCGACACAGGCTGGAAGACAGCA	1577	DB	2892	AAAAAGGAGGACAGTGTAGAAATCCCTCAGAGGAGGAAAAACCATTTTATTCAGTG	2951
DB	1812	GCCCGTGATCAGAGGCTCAGTGCGGCTGCACCTGTCCGACACAGGCTGGAAGACAGCA	1871	QY	2658	AATTACATCTCTCTGTTCTTAAAAAGCAAGTGTCTTTGGTGTGGAGACAAATTC	2717
QY	1578	ATAAGCTCAAGGCTTCTCTCTCTGGATATCAAAATCAGTTTCAATTCAGCCACATGG	1637	DB	2952	AATTACATCTCTCTGTTCTTAAAAAGCAAGTGTCTTTGGTGTGGAGACAAATTC	3011
DB	1872	ATAAGCTCAAGGCTTCTCTCTCTGGATATCAAAATCAGTTTCAATTCAGCCACATGG	1931	QY	2718	CCTACCAATTTTCAAGTTGTGCTACTAAGAGATCTCAAAATTTAGTCTTTGTCCGACCC	2777
QY	1638	CAGATCTCTTACATGGCTTCTCTCTCATCAGAGATGCTTTTGAATPACTACAACTTCCA	1697	DB	3012	CCTACCAATTTTCAAGTTGTGCTACTAAGAGATCTCAAAATTTAGTCTTTGTCCGACCC	3070
DB	1932	CAGATCTCTTACATGGCTTCTCTCTCATCAGAGATGCTTTTGAATPACTACAACTTCCA	1991	QY	2778	TTCCATAGTACACCTTAGCGCTGAGACTGAGCGAGCTTTGGGGTTCAGTAGGTAGACCT	2837
QY	1698	CTACTCTGATGGGACCAAGCTATGCGAGTTCTCGCTGTTCAGGAATCTATCGGAGC	1757	DB	3071	TTCCATAGTACACCTTAGCGCTGAGACTGAGCGAGCTTTGGGGTTCAGTAGGTAGACCT	3130
DB	1992	CTACTCTGATGGGACCAAGCTATGCGAGTTCTCGCTGTTCAGGAATCTATCGGAGC	2051	QY	2838	GTTAGGACACAGAGCTTAGTGTAAATCCAAAGAGAAATGATCTCTATCCAAAGCTGATTCAC	2897
QY	1758	AGACTCCGAAACCAAGTCTGATAGGAGGAGCAGGATCCCAAGAGGCTGCAGACCG	1817	DB	3131	GTTAGGACACAGAGCTTAGTGTAAATCCAAAGAGAAATGATCTCTATCCAAAGCTGATTCAC	3190
DB	2052	AGACTCCGAAACCAAGTCTGATAGGAGGAGCAGGATCCCAAGAGGCTGCAGACCG	2111	QY	2898	AAACCCACGCTACCTGACAGCGGAGGACACGAGCATCACTCTGCTGGACGACCAATTA	2957
QY	1818	CCAGGCTTTACAGACGACAGCAAGCGATTGCAATTCGGTTCAGAACCCAGCAGTGCCA	1877	DB	3191	AAACCCACGCTACCTGACAGCGGAGGACACGAGCATCACTCTGCTGGACGACCAATTA	3250
DB	2112	CCAGGCTTTACAGACGACAGCAAGCGATTGCAATTCGGTTCAGAACCCAGCAGTGCCA	2171	QY	2958	GGGGCTTTGCCAGGTTCTACTTTAGACCAAAACCCAGTACCTCAGACAGGAAAGTCGGGC	3017
QY	1878	CCGCCACAGGTCCTTTTATCTCACTGCAATGCAAGTGGAGGCTGGAGGACATTTACC	1937	DB	3251	GGGGCTTTGCCAGGTTCTACTTTAGACCAAAACCCAGTACCTCAGACAGGAAAGTCGGGC	3310
DB	2172	CCGCCACAGGTCCTTTTATCTCACTGCAATGCAAGTGGAGGCTGGAGGACATTTACC	2231	QY	3018	TTTGACCACTACCATATCTGTGTAGCCCATTTTCTTAGGCAATTTGTGAATAGGTAGCTA	3077
QY	1938	ACACAGCTTCTTTTGGGCTTTTCCACGAGCAGCAGCACTTCAAGAGTCTGTGGCC	1997	DB	3311	TTTGACCACTACCATATCTGTGTAGCCCATTTTCTTAGGCAATTTGTGAATAGGTAGCTA	3370
DB	2232	ACACAGCTTCTTTTGGGCTTTTCCACGAGCAGCAGCACTTCAAGAGTCTGTGGCC	2291	QY	3078	GTCACTTTTTCAGACCAATTCAAACTGTCTATGCACAAATTTCCCGTGGCCCTTAGTGG	3137
QY	1998	TGGGCTTAAAGGCTGGGACCTGGATATCTTGGGCCCCCAGACCTCTACCCCTTCCCTGA	2057	DB	3371	GTCACTTTTTCAGACCAATTCAAACTGTCTATGCACAAATTTCCCGTGGCCCTTAGTGG	3430
DB	2292	TGGGCTTAAAGGCTGGGACCTGGATATCTTGGGCCCCCAGACCTCTACCCCTTCCCTGA	2351	QY	3138	AGATAATTTTTTTTTTCTCTCAGCTTTATGAAGAGGAGGAAACTGTCTAGGATTCAGCT	3197
QY	2058	CCAGCAGCTGGTATTTTGGCAACAGATCTCACTTCTACTCTGCTCAGCCATCTACG	2117	DB	3431	AGATAATTTTTTTTTTCTCTCAGCTTTATGAAGAGGAGGAAACTGTCTAGGATTCAGCT	3490
DB	2352	CCAGCAGCTGGTATTTTGGCAACAGATCTCTCACTTCTACTCTGCTCAGCCATCTAGC	2411	QY	3198	GAACCAACGAGACCTGGCAACATCAAGTTTAAAGCTTAAAGGTTGGGAGGCTTAACAGTCT	3257
QY	2118	GAGGAGTGCAGTTTACTCTGCTACAGCTGAGGAGCTGCGACCTTGGGAGACCAAG	2177	DB	3491	GAACCAACGAGACCTGGCAACATCAAGTTTAAAGCTTAAAGGTTGGGAGGCTTAACAGTCT	3550
DB	2412	GAGGAGTGCAGTTTACTCTGCTACAGCTGAGGAGCTGCGACCTTGGGAGACCAAG	2471	QY	3258	ACCTCCCTCTTTGTAAATCAAGAAATTTTAAATTTGGGATTTGTCAATCTTTAAATATAA	3317
QY	2178	TCTATTCTGTGCGAGGCGGACAGCCAAAGTGCAGAGCTGACTCGCGCGGAGCTGGC	2237				

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Patent No. US20020034807A1

GENERAL INFORMATION:

APPLICANT: Meyers, Rachel A.

TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY

FILE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR

FILE REFERENCE: 10448-030002

CURRENT APPLICATION NUMBER: US/09/816,494

CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: US 60/191,858

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 3544

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (589)...(2583)

i-09-816-494-1

Query Match 88.5%; Score 2950; DB 9; Length 3544;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

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Db 2204 GGCATCGGATATTTGGGCCCCCAGACCTTACACCTTCCCTGACACAGCAGCTGTATT 2263
QY 2073 TTGCCACAGAGTCTCAGACTTCTACTCTGCTCAGCAGCTCTACGGAGCAGTGCAGTT 2132
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RESULT 6

US-10-377-072-25

; Sequence 25, Application US/10377072

; Publication No. US20040009501A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals Inc.

; APPLICANT: Curtis, Rory A.J.

; APPLICANT: Logan, Thomas Joseph

; APPLICANT: Gluckmann, Maria A.

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Williamson, Mark J.

; APPLICANT: Rudolph-Owen, Laura A.

; APPLICANT: Chun, Miyoung

; APPLICANT: Tsai, Fong-Ving

; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,

; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES

; FILE REFERENCE: AND USES THEREFOR

; CURRENT APPLICATION NUMBER: US/10/377,072

; CURRENT FILING DATE: 2003-02-27

; PRIOR APPLICATION NUMBER: US 09/895,860

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/215,370

; PRIOR FILING DATE: 2000-06-29

; PRIOR APPLICATION NUMBER: US 09/723,806

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 60/187,455

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: US 09/843,297

; PRIOR FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: US 60/199,801

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: US 09/861,801

; PRIOR FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: US 60/205,508

; PRIOR FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: US 09/816,494

; PRIOR FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: US 09/815,419

; PRIOR FILING DATE: 2001-03-22

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 3544

; TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (589) ... (2586)

;10-377-072-25

Query Match 88.5%; Score 2950; DB 16; Length 3544;

Best Local Similarity 95.0%; Pred. No. 0;

Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

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RESULT 9

US-10-257-026-1
 ; Sequence 1, Application US/10257026
 ; Publication No. US2004008659A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Merck Patent GmbH
 ; TITLE OF INVENTION: New dual specificity phosphatase
 ; FILE REFERENCE: DUSP10XDM5
 ; CURRENT APPLICATION NUMBER: US/10/257,026
 ; CURRENT FILING DATE: 2003-11-07
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 3059
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (127)..(2121)
 US-10-257-026-1

Query Match 81.3%; Score 2710; DB 17; Length 3059;
 Best Local Similarity 94.6%; Pred. No. 0;
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US-10-296-115-520				
; Sequence 520, Application US/10296115				
; Publication No. US20040053248A1				
; GENERAL INFORMATION:				
; APPLICANT: Hyseq Inc				
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides				
; FILE REFERENCE: 784PCT				
; CURRENT APPLICATION NUMBER: US/10/296,115				
; CURRENT FILING DATE: 2002-11-18				
; PRIOR APPLICATION NUMBER: US09/488,725				
; PRIOR FILING DATE: 2000-01-21				
; PRIOR APPLICATION NUMBER: US09/552,317				
; PRIOR FILING DATE: 2000-04-25				
; NUMBER OF SEQ ID NOS: 1478				
; SEQ ID NO 520				
; LENGTH: 2966				
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; ORGANISM: Homo sapiens				
; FEATURE:				
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; LOCATION: (1) - (2966)				
; OTHER INFORMATION: n = a,t,c,g or g				
US-10-296-115-520				
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Best Local Similarity 94.3%; Pred. No. 0;				
Matches 2789; Conservative 0; Mismatches 3; Indels 165; Gaps 2;				
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QY 1336 GCTGCACTTGGAGAGCCAAATGAACCTGTCTCCCTGCTGCTCAGAGGGTGGACAGAAAG 1395
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Db 1021 CGAGAGCCCTCAGTCCACCTGTGCGCACTCTGTACTCTCAGAGCCAGGAGCAAG 1080
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QY 2056 GACACAGAGCTGTTATTTTGCACAGAGTCTCTCACATTTCTACTCTGCTCAGCATCTA 2115
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QY 2116 CGAGGCTGCTCAGTACTCTGCTACAGCTGACGCGAGCTGCCACTTCGGGAGACCA 2175
Db 1741 CGAGGCTGCTCAGTACTCTGCTACAGCTGACGCGAGCTGCCACTTCGGGAGACCA 1800
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QY 2296 AGAGAGCATCATGTTCAGAGACAGCTCAGCGGAGAGCTGGGAAAGTGGGAGCTCAGCT 2355
Db 1921 AGAGAGCATCATGTTCAGAGACAGCTCAGCGGAGAGCTGGGAAAGTGGGAGCTCAGCT 1980
QY 2356 TAGCTTTTTCGGGAGCAGTGAATTCATTTAGGCTCTCTGAGAGAGAGACACTTTGCTACT 2415
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961 CTAGTCCCTACTGCATTCTCAGCCTTGCTTACTGTGGCAACATGGGCCAACCGA 1020

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942		1001
1081	CAGAAATGGATTTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTCAGCTTTATC	1140
1082		1141
1001	CCCGAGTCTCATTTCTCCGCTGTGCTGTGAATGACAGAGCTTTGTGAGAAAAATTTTGGCG	1060
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1142		1201

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 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3381
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 673
 ; LENGTH: 2102
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-094-749-673

Query Match 52.9%; Score 1762.4; DB 16; Length 2102;
 Best Local Similarity 92.2%; Pred. No. 0;
 Matches 1937; Conservative 0; Mismatches 1; Indels 164; Gaps 1;

QY	507	TACATCATCTGCGCAATTAAGAGAGGAGGTCGGAAAGAGGACTTATTGTTGTCATGCG	566
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QY	567	CCATGAGATGATTGGAACCTCAAAATTGTTACTGAGAGGTTGGTGCTCTGCTGGAAGTGG	626
DB	61	CCATGAGATGATTGGAACCTCAAAATTGTTACTGAGAGGTTGGTGCTCTGCTGGAAGTGG	120
QY	627	AACGGAAGAAGTGTCTAAATTGNTAGCGGCCATTTTGTGGAATACATATACATCCACAT	686
DB	121	AACGGAAGAAGTGTCTAAATTGNTAGCGGCCATTTTGTGGAATACATATACATCCACAT	180
QY	687	TTTGGAGCCATTATATCACTGCTCAAGCTTATGAGCGAGGTTGCAACAGACAA	746
DB	181	TTTGGAGCCATTATATCACTGCTCAAGCTTATGAGCGAGGTTGCAACAGACAA	240
QY	747	AGTGTAAATACAGAGCTCATCCAGCATTCAGGAAACATAGGTTGACATTTGTCAG	806
DB	241	AGTGTAAATACAGAGCTCATCCAGCATTCAGGAAACATAGGTTGACATTTGTCAG	300
QY	807	TCAGAGGTTGTAGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTCTTCAAGCTG	866
DB	301	TCAGAGGTTGTAGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTCTTCAAGCTG	360
QY	867	TTTTCTCACTGTAATCTGGGTAAACTGGAGAGGCTTCAACTGTTTCACTGCTTGC	926
DB	361	TTTTCTCACTGTAATCTGGGTAAACTGGAGAGGCTTCAACTGTTTCACTGCTTGC	420
QY	927	-----	926
DB	421	AGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCTCTGTGAGGAAATCCACTCT	480
QY	927	-----	926
DB	481	AGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAATTTGGGCCAACCTAAT	540
QY	927	-----	926
DB	541	TCCTTCCCAATCTTTATCTGGCTGCCGAGATGTCCTCAACAGAGGCTGATGACGA	600
QY	943	GAATGGGATGGTTAGTTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGATTTATCCC	1002
DB	601	GAATGGGATGGTTAGTTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGATTTATCCC	660
QY	1003	CGAGTCTCAATTTCTCGGCTGCTGTAATGACAGCTTTTGTGAGAAATTTTGGCCGTG	1062
DB	661	CGAGTCTCAATTTCTCGGCTGCTGTAATGACAGCTTTTGTGAGAAATTTTGGCCGTG	720
QY	1063	GTTCGACAAATCAGTAGATTTCATTGAGAAACAAAGCCTCAATGATGTTGTTCTAGT	1122
DB	721	GTTCGACAAATCAGTAGATTTCATTGAGAAACAAAGCCTCAATGATGTTGTTCTAGT	780
QY	1123	GCACTGTTTGTAGCTGGGATCTCCCGCTCCGCCCAATCGCTATCGCTTATCGCTAATG	1182
DB	781	GCACTGTTTGTAGCTGGGATCTCCCGCTCCGCCCAATCGCTATCGCTTATCGCTAATG	840
QY	1183	GATGACATGCTTTAGATGAAGCTTACAGATTTGTGAGAAAGAAAGACCTTACTATATC	1242

QY	1243	TCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAAGAACGAC	1302
DB	901	TCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGATTAAAGAACGAC	960
QY	1303	TGAGCATCAGGCGCAAGAGCAAACTCAAGCTGCTGCACTTGAGAGAGCCAAATGAACC	1362
DB	961	TGAGCATCAGGCGCAAGAGCAAACTCAAGCTGCTGCACTTGAGAGAGCCAAATGAACC	1020
QY	1363	TGTCCTGCTGCTCAGAGGGTGACAGAAAAGGAGACGCCCTCAGTCCACCTCTGC	1422
DB	1021	TGTCCTGCTGCTCAGAGGGTGACAGAAAAGGAGACGCCCTCAGTCCACCTCTGC	1080
QY	1423	CGACTCTGTACTCAGAGGCGAGCAAAAGGCCGCTGCATCCCGCCAGCGTGCACG	1482
DB	1081	CGACTCTGTACTCAGAGGCGAGCAAAAGGCCGCTGCATCCCGCCAGCGTGCACG	1140
QY	1483	CGTCCCGAGCGTGCAGCGCTGCTGTTAGAGGACAGCCCGCTGCTACAGGCGCTCAGTGG	1542
DB	1141	CGTCCCGAGCGTGCAGCGCTGCTGTTAGAGGACAGCCCGCTGCTACAGGCGCTCAGTGG	1200
QY	1543	GCTGCACCTGTCGCGACAGCGCTGGAAGACAGCAATAAGCTCAAGGTTCTCTCTCT	1602
DB	1201	GCTGCACCTGTCGCGACAGCGCTGGAAGACAGCAATAAGCTCAAGGTTCTCTCTCT	1260
QY	1603	GGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGGCTTCTCTC	1662
DB	1261	GGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGGCTTCTCTC	1320
QY	1663	ATCAGAGATGCTTTTGAATACACTACAAACCTTCCACTACTCTGATGGGACCAACAGCT	1722
DB	1321	ATCAGAGATGCTTTTGAATACACTACAAACCTTCCACTACTCTGATGGGACCAACAGCT	1380
QY	1723	ATGCCAGTTCTCCCTGTTTCAAGAACTATCGAGACAGACTCCCGAAACCAAGTCTGTATAA	1782
DB	1381	ATGCCAGTTCTCCCTGTTTCAAGAACTATCGAGACAGACTCCCGAAACCAAGTCTGTATAA	1440
QY	1783	GGAGAGACCGAGCATCCCAAGAGCTGCGAGCGCCAGCGCTTTCAGAGCGCAGACAA	1842
DB	1441	GGAGAGACCGAGCATCCCAAGAGCTGCGAGCGCCAGCGCTTTCAGAGCGCAGACAA	1500
QY	1843	GCGATTGCATTCGCTCAGAAACCGAGCAGTGGCAGCCGCGCAGAGTCCCTTTTATCTCC	1902
DB	1501	GCGATTGCATTCGCTCAGAAACCGAGCAGTGGCAGCCGCGCAGAGTCCCTTTTATCTCC	1560
QY	1903	ACTGCATCGAAGTGGAGCGTGGAGGACAATTAACACACAGCTTCTTTTGGCCTTTC	1962
DB	1561	ACTGCATCGAAGTGGAGCGTGGAGGACAATTAACACACAGCTTCTTTTGGCCTTTC	1620
QY	1963	CACAGCGCAGCAGCACTCTAGAAAGTCTGCTGGCTGGCGCTTAAGGGCTGGCAGCTCGGA	2022
DB	1621	CACAGCGCAGCAGCACTCTAGAAAGTCTGCTGGCTGGCGCTTAAGGGCTGGCAGCTCGGA	1680
QY	2023	TATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACCCAGCAGCTGGTATTTTGGCCACAGA	2082
DB	1681	TATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACCCAGCAGCTGGTATTTTGGCCACAGA	1740
QY	2083	GTCCTCACACTTCTACTCTGCTCAGCAATCTACGGAGGAGTGCACAGTACTCTGCTCTA	2142
DB	1741	GTCCTCACACTTCTACTCTGCTCAGCAATCTACGGAGGAGTGCACAGTACTCTGCTCTA	1800
QY	2143	CAGCTGACCGCAGCTGCGCACTTTCGAGAGCAAGTCTATTTGTGCGCAGGCGGAGAA	2202
DB	1801	CAGCTGACCGCAGCTGCGCACTTTCGAGAGCAAGTCTATTTGTGCGCAGGCGGAGAA	1860
QY	2203	GCGAAGTACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGGCCCTTTTGAAGCA	2262
DB	1861	GCGAAGTACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGGCCCTTTTGAAGCA	1920
QY	2263	GTTTAAACGCGAAGCTGCGCAATTTGGAGAGAGCATCATGTTCAGAGAACAGTTC	2322
DB	1921	GTTTAAACGCGAAGCTGCGCAATTTGGAGAGAGCATCATGTTCAGAGAACAGTTC	1980

QY	1313	GGGCCAAAGAGCAAACTCAAGCTGTCTGCACTCTGGAGAGGCCAAATGAACCTGTCCCTGCCT	1377
DB	1021	GGGGCCAAAGAGCAAACTCAAGCTGTCTGCACTCTGGAGAGGCCAAATGAACCTGTCCCTGCCT	1080
QY	1373	GTCTCAGAGGGTGGACAGAAAGCGAGACGCCCTCAGTCCACCCCTGTGCGGACTCTGCCT	1432
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QY	1433	ACCTCAGAGGCGAGCAGGACAAAGGCCCGGTGCATCCCGCCACGCTGCCACGCTGCCCGACG	1492
DB	1141	ACCTCAGAGGCGAGCAGGACAAAGGCCCGGTGCATCCCGCCACGCTGCCACGCTGCCCGACG	1200
QY	1493	GTGCAGCCGTCTCGCTTTAGAGGACAGCCCGCTGTGTACAGCGCTCAGTGGGCTGCACCTG	1552
DB	1201	GTGCAGCCGTCTCGCTTTAGAGGACAGCCCGCTGTGTACAGCGCTCAGTGGGCTGCACCTG	1260
QY	1553	TCCCGACAGCGCTGGAGACAGCAATAAGCTCAAGGTTCTTCTCTCTCTGGATATCAAA	1612
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QY	1613	TCAGTTTTCATATTCAGCCAGCATGGCAGCATCCCTTACATGCTCTTCTCTCATCAGAAGAT	1672
DB	1321	TCAGTTTTCATATTCAGCCAGCATGGCAGCATCCCTTACATGCTCTTCTCTCATCAGAAGAT	1380
QY	1673	GCTTTGGAAATACTAAACCTTCCACTACTCTCTGGATGGGACCAACAGCTATGCCAGTTC	1732
DB	1381	GCTTTGGAAATACTAAACCTTCCACTACTCTCTGGATGGGACCAACAGCTATGCCAGTTC	1440
QY	1733	TCCCTGTTCAGGAACTATTCGGAGCAGATCCCCGAAAACAGCTCTGTATAGGAGGAGGCC	1792
DB	1441	TCCCTGTTCAGGAACTATTCGGAGCAGATCCCCGAAAACAGCTCTGTATAGGAGGAGGCC	1500
QY	1793	AGCATCCCAAGAGAGCTGCAGACCGCCAGCGCTTCAGACAGCCAGAGCAAGCCATGGCAT	1852
DB	1501	AGCATCCCAAGAGAGCTGCAGACCGCCAGCGCTTCAGACAGCCAGAGCAAGCCATGGCAT	1560
QY	1853	TCGGTTCAGAAACCCAGCAGCTGGCAACCGCCAGAGGTCCTTTTATCTCCACCTGCATCGA	1912
DB	1561	TCGGTTCAGAAACCCAGCAGCTGGCAACCGCCAGAGGTCCTTTTATCTCCACCTGCATCGA	1620
QY	1913	AGTGGGAGCGTGGAGGCAATATACCAACACAGCTTCCTTTTCGGCCCTTCCACAGCCAG	1972
DB	1621	AGTGGGAGCGTGGAGGCAATATACCAACACAGCTTCCTTTTCGGCCCTTCCACAGCCAG	1680
QY	1973	CAGCACCTCAGAACTCTGCTGGCCCTTAAAGGCTGGCACTCGGATATCTTTGGCC	2032
DB	1681	CAGCACCTCAGAACTCTGCTGGCCCTTAAAGGCTGGCACTCGGATATCTTTGGCC	1740
QY	2033	CCCCAGACCTTACCCCTTCCCTGCACAGCAGCTGGTATTTTGGCCACAGAGTCTCCACAC	2092
DB	1741	CCCCAGACCTTACCCCTTCCCTGCACAGCAGCTGGTATTTTGGCCACAGAGTCTCCACAC	1800
QY	2093	TTCTACTCTGCTCAGCCATCTACGGAGGCACTGCCAGTTCCTCTCCTACAGCTGCAGC	2152
DB	1801	TTCTACTCTGCTCAGCCATCTACGGAGGCACTGCCAGTTCCTCTCCTACAGCTGCAGC	1860
QY	2153	CAGCTGCCCATCTTGGGAGACCAAGTCTATTCTGTGGCAGGCGGAGAGCCCAAGTGAC	2212
DB	1861	CAGCTGCCCATCTTGGGAGACCAAGTCTATTCTGTGGCAGGCGGAGAGCCCAAGTGAC	1920
QY	2213	AGAGCTGACTCTGGCGGCGAGCTGGCATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGC	2272
DB	1921	AGAGCTGACTCTGGCGGCGAGCTGGCATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGC	1980
QY	2273	AGAAGCTGCCAAATGGAAATTTGGAGAGAGCATCATGTTCAGAGAACAGGTCACGGGAAG	2332
DB	1981	AGAAGCTGCCAAATGGAAATTTGGAGAGAGCATCATGTTCAGAGAACAGGTCACGGGAAG	2040
QY	2333	CTGGGGAAGAGTGGGAGTCTAGCTTTTTCGGGAGCAGCATGGAAATCATTTAGGCTCTCC	2392
DB	2041	CTGGGGAAGAGTGGGAGTCTAGCTTTTTCGGGAGCAGCATGGAAATCATTTAGGCTCTCC	2100
QY	2393	TGAGAGAAAGAGCACTGTGCTCTTCTATAGCAAAATTTTTTTTCTTGTTCACAAAAT	2452

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Db      2101 TGAGAGAAAGACACATTGTGCACTTCTATAGACAAATTTTTTTTCTGTTCCACAAAAAT 2160
QY      2453 TCCCTGTAAATCTGAAATATATATATATGTCATACATATAT 2492
Db      2161 TCCCTGTAAATCTGAAATATATATATATGTCATACATATAT 2200

RESULT 15
US-10-072-012-257
; Sequence 257, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Raetelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
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; PRIOR APPLICATION NUMBER: 60/265,517
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; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 257
; LENGTH: 2071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-257

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Query Match 51.4%; Score 1712.4; DB 13; Length 2071;
 Best Local Similarity 91.6%; Pred. No. 0;
 Matches 1906; Conservative 0; Mismatches 1; Indels 173;

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1 ACCATTACATCGTGGCAAAATTAAGAGGAGGTGGGAAAGAGGACTTATTGTTGTC 60
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61 ATGGCCCATGAGATGATTTGGAACCTCAATTTGTTACTGAGAGGTTGGTCTCTCTCGAA 120
622 AGTGGAAACGGAAGAGTCTGCTAAATGATAGCGGCCAATTTGTGGAATACAATACATCC 681
121 AGTGGAAACGGAAGAGTCTGCTAAATGATAGCGGCCAATTTGTGGAATACAATACATCC 180
682 CACATTTTGGAGGCAATTAATATCACTGCTCCAAAGCTTATGAGCGGAGGTGCAACAG 741
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301 TGCAGTCAGAAAGTGTGATTTTACATCAAGCTCCCAAGATGTTGCTCTCTCTCTTCA 360
862 GACTGTTTCTCACTGTACTTCTGGGTAAACTGGGAGAGGCTTCAACTCTGTTCACTG 921
361 GACTGTTTCTCACTGTACTTCTGGGTAAACTGGGAGAGGCTTCAACTCTGTTCACTG 420
922 CTTCG----- 926
421 CTTCGAGGTGGGTTGCTGAGTCTCTGTTGTTTCCCTGGGCTCTGTGAAGGAAATCC 480
927 ----- 926
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927 ----- AGGAGCTGATG 937
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601 CAGCAGAAATGGGATTTGTTATGTTAAATGCGCAATPACTGCTCCAAAGCTGACTTT 660
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1972 AGGTCAAGGAGAGCTGGGAAAGTGGCAGTCTAGTCTAGCTTTTGGGCGAGCATGGA 2031
2378 ATCATGTAGGTTCTCTGAGAGAGAGACACTTTGTGACTTC 2417
2032 ATCATGTAGGTTCTCTGAGAGAGAGACACTTTGTGACTTC 2071

Search completed: September 24, 2004, 07:10:24
Job time : 1935 secs

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3	844	33.6	2377	4	US-09-920-668-3	Sequence 3, Appl
4	308	11.5	2303	4	US-09-922-146-3	Sequence 3, Appl
5	289.5	10.9	1238	4	US-09-702-705-803	Sequence 803, App
6	289.5	10.9	1238	4	US-09-736-457-803	Sequence 803, App
7	289.5	10.9	1238	4	US-09-614-1248-803	Sequence 803, App
8	289.5	10.9	1238	4	US-09-671-325-803	Sequence 803, App
9	289.5	10.9	1238	4	US-09-589-184-803	Sequence 803, App
10	287	10.8	1619	4	US-09-702-705-801	Sequence 801, App
11	287	10.8	1619	4	US-09-736-457-801	Sequence 801, App
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 QY 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
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 QY 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
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RESULT 2

US-09-816-494-1
 ; Sequence 1, Application US/09816494
 ; Patent No. 6664089
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel A.
 ; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
 ; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: 10448-030002
 ; CURRENT APPLICATION NUMBER: US/09/816,494
 ; CURRENT FILING DATE: 2001-03-23
 ; PRIOR APPLICATION NUMBER: US 60/191,858
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 3544
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (589) ... (2583)
 ; US-09-816-494-1

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 Pred. No.: 1,11e-253 Length: 3544
 Score: 2606.00 Matches: 516
 Percent Similarity: 90.21% Conservative: 0
 Best Local Similarity: 90.21% Mismatches: 1
 Query Match: 97.68% Indels: 56
 DB: 4 Gaps: 1

US-09-964-277-21 (1-517) x US-09-816-494-1 (1-3544)

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49	LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys	68
753	AAC--CACTTTCAAGGACACTATCAGTACAAAGTCATCCCATCGAAGATAACCAACAAG	809
69	GluLysIleLeuProThrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer	88
810	GCGACATCAGCTCTCGTTTCATGAAGCCATAGAGTACATCGATCGCGTGAAGGACTGC	869
89	AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle	108
870	CGTGGCGCGTGTGTGTGCATCTGCCGGCGGCATCTCGCGTGGCCACCATCTGCCTG	929
109	AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu	128
930	GCCTACTGATGATGAAGAAACGGGTGAGGCTGGAGAGGCCCTCGAGTTCGTTAAGCAG	989
129	LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys	148
990	CGCGCGCAGCATCATCTCGCCCACTTCAGCTTCATGGGGCAGCTGCTCGAGTTCGAGTCC	1049
149	LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeu	168
1050	CAGTGTCTGCCACGTCCTGTCTCGGAGGCTGTAGC-----	1088
169	GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro	188
1089	-----CCCTCGGACCCCTG-----GGGAGCGGGGACAGACCCCC	1124
189	LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis	208
1125	GCCACCC-----ACCTCGAGTTCGTCTTCAGCTTCCGATC-----	1163
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229	ValGlnAlaLeuSer	233
1218	ACCACCTCTCCCGAC	1232

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RESULT 6
US-09-736-457-803
; Sequence 803, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478CL5
; CURRENT APPLICATION NUMBER: US/09/736.457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-803

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Db 1218 ACCACCTCTCCAGC 1232
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US-09-702-705-801
; Sequence 801, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-801

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Score: 287.00 Matches: 73
Percent Similarity: 55.02% Conservative: 42
Best Local Similarity: 34.93% Mismatches: 69
Query Match: 10.76% Indels: 25
DB: 4 Gaps: 6

US-09-964-277-21 (1-517) x US-09-702-705-801 (1-1619)
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Qy 129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
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Qy 226 rProLeuValGlnAlaLeuSerGly 234
Db 900 -CCAGCTGTTAGCGCCCTCGGG 923

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US-09-736-457-801
; Sequence 801, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-801

Alignment Scores:
Pred. No.: 5,68e-19 Length: 1619
Score: 287.00 Matches: 73
Percent Similarity: 55.02% Conservative: 42
Best Local Similarity: 34.93% Mismatches: 69
Query Match: 10.76% Indels: 25
DB: 4 Gaps: 6

US-09-964-277-21 (1-517) x US-09-736-457-801 (1-1619)
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Db 365 AGAGACATGCTGGAGCCCTGGGCATCAGCGCTCTGTTGAATGCTCTCGAGTGCCTCA 424
Qy 49 LysProAspPheLeuProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
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Qy 69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
Db 482 GCCGACATCAGCTCTGTTTCATGGAAGCCATAGAGTACATGATGCCGTGAAGACTGTC 541
Qy 89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
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Db 602 GCCTACCTGATGATCAAGAAACGGGTGAGGCTGAGGAGGCTTTCAGTTCGTTAAGCAG 661
Qy 129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
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RESULT 13
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; Sequence 801, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-801

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[illegible]

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Alignment Scores:
Pred. No.: 5,69e-19 Length: 1619
Score: 287.00 Matches: 73
Percent Similarity: 55.02% Conservative: 42
Best Local Similarity: 34.93% Mismatches: 69
Query Match: 10.76% Indels: 25
DB: Gaps: 6
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US-09-964-277-21 (1-517) x US-09-671-325-801 (1-1619)

Qy 29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 AGAGACATGCTGGAGCGCCTGGCGCATCACGGCTCTGTTGAATGTCTCTCGAAGTCCCA 424
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Qy 49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 AAC---CNCITTGAGGACACTATCATGTCAGTGCATCCCGAGATGAACACAG 481
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88

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set Local Similarity: 34.93% Mismatches: 69
Query Match: 10.76% Indels: 25
3: 4 Gaps: 6

3-09-964-277-21 (1-517) x US-09-702-705-825 (1-2064)

29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
1036 AGAGACATGCTGGAGCCCTGGGCATCACGGCTCTGTGAATGCTCTCTCGGACTGCCCA 1095
49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
1096 AAC---CACTTGAAGGACACTATCAGTACAGTGCATCCCACTGGAGAGATAACCAACAG 1152
69 GluLysIleLeuProThrPheLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
1153 GCCGACATCAGCTCTCTGTTGATGCAAGCCATAGAGTACATGATCCGCTGAAGGACTGC 1212
89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
1213 CGTGGCGCGTCTGTCGTCATGCCAGGGCGGCATCTCGCGTCCGCCACCATCTGCGCTG 1272
109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
1273 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGAGGCCCTTCAGTTGCTTAAGCAG 1332
129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
1333 CGCCGACGATCATCTGCCCACTTCAGCTTCATGGGCGAGCTGCTGAGTTCGAGTCC 1392
149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeu 168
1393 CAGGTGCTGGCCACGCTCTGCTGCTGGAGGCTGTAGC----- 1431
169 GluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrPro 188
1432 -----CCCTCGGACCCCTG-----CGGAGCGGGCGCAAGACCCCC 1467
189 LeuSer-ProProCysAlaAspSerAlaThr-----SerGluAlaAlaGlyGlnArgPr 206
1468 GCCACCCCACTCGCAGTCTGCTTCAGCTTCGCGTCTCGTGGGCGTGCACCTCGGCC 1527
206 oValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuLysPse 226
1528 C-----CCAGAGCGCTGCCCTACCTGCACAGCCCATCACCACCTCTC----- 1570
226 rProLeuValGlnAlaLeuSerGly 234
1571 -CCAGCTGTAGAGCGCCCTGGGG 1594

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GenCore version 5.1.6
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4 protein - nucleic search, using frame_plus_p2n model

on: September 24, 2004, 06:38:37; Search time 714 Seconds
(without alignments)
3667.477 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

sarched: 3337386 seqs, 2532474682 residues

tal number of hits satisfying chosen parameters: 6674772

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ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:

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14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:

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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:

17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:

18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	4.86e-266	2668.00	3332	US-09-964-277-20	Sequence 20, Appli
2	2668.00	517	3332	US-09-964-277-20	Sequence 3, Appli
3	100.00%	Conservative:	0		Sequence 27, Appli

ALIGNMENTS

RESULT 1

US-09-964-277-20
; Sequence 20, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Bo
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964, 277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 3332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-20

Alignment Scores:	4.86e-266	Length:	3332
Pred. No.:	2668.00	Matches:	517
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-964-277-21 (1-517) x US-09-964-277-20 (1-3332)

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 DB 842 ATGTTGCCCTCTCTCTCTCAGACTGTTTCTCTACTGTACTTCTGGGTAACCTGAGAGA 901
 QY 21 AlaSerThrLeuPheThrCysLeuGlnGluLeuMetGlnGlnAsnGlyIleGlyTyrVal 40
 DB 902 GCTTCAACTCTGTTTCACTCTGTTGAGGAGCTGATGCAGAGATGGGATTGGTTATGTG 961
 QY 41 LeuAsnAlaSerAsnThrCysProLysProLysProAspPheIleProGluSerHisPheLeuArg 60
 DB 962 TTAATATGCCAGCAATACCTGTCCTCAAGCCCTGACTTTATCCCGAGTCTCATTTCTCTGGT 1021
 QY 61 ValProValAsnAspSerPheCysGlyLysIleLeuProTrpLeuAspLysSerValAsp 80
 DB 1022 GTGCCCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCTGGTGTGACAAATCAGTAGAT 1081
 QY 81 PheIleGluLeuAlaLysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIle 100
 DB 1082 TTCAATTGAGAGCAAGCAAGCCCTCCATGATGTTCTAGTGCACCTGTTTAGCTGGATC 1141
 QY 101 SerArgSerAlaThrIleAlaIleAlaIleAlaIleMetLysArgMetAspMetSerLeuAsp 120
 DB 1142 TCCCGCTCCGCCACCATCTATCGCTACATCATGAGAGGATGACATGCTTTAGAT 1201
 QY 121 GluAlaTyrArgPheValLysArgProThrIleSerProAsnPheAsnPheLeu 140
 DB 1202 GAAGCTTACAGATTCTGTGAAGAAAAGACCTACTATATCTCCAACTTCAATTTCTGT 1261
 QY 141 GlyGlnLeuLeuAspTyrGlyLysIleLysAsnGlnThrGlyAlaSerGlyProLys 160
 DB 1262 GGCCAACTCTGTGACTATGAGAGAGAGATTAGACCAGCTGGAGCATCAGGGCCCAAG 1321
 QY 161 SerLysLeuLysLeuLeuHisLeuGlyLysProAsnGluProValProAlaValSerGlu 180
 DB 1322 AGCAAACTCAAGCTGTGACCTCGGAGAGCCAAATGAACCTGCTCCTGCTCTCAGAG 1381
 QY 181 GlyGlyGlnLysSerGluThrProLeuSerProCysAlaAspSerAlaThrSerGlu 200
 DB 1382 CGTGGACAGAAAGCAGACGCGCTCAGTCCACCTGTGCGGACTCTGCTACCTCAGAG 1441
 QY 201 AlaAlaGlyLysArgProValHisProAlaSerValProSerValGlnPro 220
 DB 1442 GCAGCAGAGCAAGGCCCTGTGATCCCGCAGCGTCCAGCGTCCCGAGCGTGGAGCG 1501
 QY 221 SerLeuLeuGluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAsp 240
 DB 1502 TGCTGTTTAGAGCAGACCGCTGTTGACAGAGCTCAGTGGGCTGCACCTGTCCGAGAC 1561
 QY 241 ArgLeuGluAspSerAsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSer 260
 DB 1562 AGGCTGGAAGACAGCAATAAGCTCAAGCGTCTCTCTCTGATATCAATCAAGTTTCA 1621
 QY 261 TyrSerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGlu 280
 DB 1622 TATTACGAGCAGATGCGAGCATCTTACATGCTGCTTCTCTCATCAGAGATGCTTTGAA 1681
 QY 281 TyrTyrLysProSerThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProVal 300
 DB 1682 TACTACAAACCTTCCACTACTCTGGATGGGACCAACAGCTATGCCAGTCTCCCTGT 1741
 QY 301 GlnGluLeuSerGlnGlnThrProGluThrSerProAspLysGluLeuAlaSerIlePro 320
 DB 1742 CAGGAATATCGAGCAGACTCCCGAAACCACTCTGATAGAGAGCAACCCAGCATCC 1801
 QY 321 LysLysLeuGlnThrAlaArgProSerAspSerGlnSerLysArgLeuHisSerValArg 340
 DB 1802 AAGAACTGACAGCCGCGGCTTTCAGACAGCAGAGCAAGCGATTGATTCGCTCGA 1861

QY 341 ThrSerSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySer 360
 DB 1862 ACCAGCAGCTGGCAGCGCCAGAGGTCCCTTTTATCTTCACTGCATCGAAGTGGGAGC 1921
 QY 361 ValGluAspAsnTyrHisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeu 380
 DB 1922 GTGGAGGACAATTAACCAACAGCTTCTTTTTCGGCTTTCACAGCAGCAGCAGCCTC 1981
 QY 381 ThrLysSerAlaGlyLeuGlyLysGlyTyrHisSerAspIleLeuAlaProGlnThr 400
 DB 1982 ACGAAGTCTGTGGCTTGAAGGCTTGAAGGCTGGCACTGGGATATCTTGGCCCCCAGACC 2041
 QY 401 SerThrProSerLeuThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSer 420
 DB 2042 TCTACCCCTTCCCTGACAGCAGCTGGTATTTTCCACAGAGTCTCTACACTTCTACTCT 2101
 QY 421 AlaSerAlaIleTyrGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuPro 440
 DB 2102 GCCTCAGCACTACGAGGAGGAGTGCAGTTACTCTGCTTACAGCTGCAGCAGCTGCC 2161
 QY 441 ThrCysGlyAspGlnValTyrSerValArgArgGlnLysProSerAspArgAlaAsp 460
 DB 2162 ACTTGGGAGACCAAGTCTATTCTGTGCGCAGCGGCGAGAGCAAGTGCAGAGAGCTGAC 2221
 QY 461 SerArgArgSerTrpHisGluGluSerProPheGluLysGlnPheLysArgArgSerCys 480
 DB 2222 TCGCGCGGAGCTGGCATGAAGAGAGGCCCCCTTTGAAAGCAGTTTAAACGAGAGCTG 2281
 QY 481 GlnMetGluPheGlyGluSerIleMetSerGluAsnArgSerArgGluLeuLys 500
 DB 2282 CAAATGGATTTGGAGAGAGCATCATGTACAGAGACAGCTCAGCGAGAGCTGGGAGAA 2341
 QY 501 ValGlySerGlnSerSerPheSerGlySerMetGluIleIleGluValSer 517
 DB 2342 GTGGGAGCTAGTCTAGCTTTTCGGGAGCATGGAATCATTTAGAGTCTCC 2392

RESULT 2

US-09-816-494-3
 ; Sequence 3, Application US/09816494
 ; Patent No. US2002034807A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel A.
 ; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
 ; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: 10448-030002
 ; CURRENT APPLICATION NUMBER: US/09/816,494
 ; CURRENT FILING DATE: 2001-03-23
 ; PRIOR APPLICATION NUMBER: US 60/191,858
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1998
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-816-494-3

Alignment Scores:
 Score: 6.18e-260 Length: 1998
 Percent Similarity: 2606.00 Matches: 516
 Best Local Similarity: 90.21% Conservative: 0
 Query Match: 97.68% Mismatches: 1
 DB: 9 Indels: 56
 Gaps: 1

US-09-964-277-21 (1-517) x US-09-816-494-3 (1-1998)

QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
 DB 281 ATGTTGCCCTCTCTCTCTCAGACTGTTTCTCTACTGTACTTCTGGTAAACTGGAGAGA 340
 QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29

341 GCTTCAACTCTGTTCCACCTGCTTGCA-GGTGGGTTTGTGAGTTCTCTCTGTTTTCCT 399
29 ----- 29
400 GGCCTCTGTGAAGGAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 459
29 ----- 29
460 GTTGCCAACTTTGGGCCAACCGAATCTTCCCAATCTTTATCTTTGGCTGCCAGCAGAT 519
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520 GTCTCTCAACAGGAGCTGATGAGCAGAAATGGGATTTGGTTATGTGTAAATGCCAGCAAT 579
46 ThrCysProLysProAspPheLeuProGlnSerHisPheLeuArgValProValAnasp 65
580 ACCTGTCCAAAGCCCTGACTTTATCCCGAGTCTCAATTTCTCGGTGTGCTGTGAATGAC 639
66 SerPheCysGluLeuLeuLeuProTirLeuAspLysSerValAspPheLeuGlyValAla 85
640 AGCTTTTGTGAGAAATTTTGGGTGGTGGCAATCAGTAGATTTTCATTGAGAAAGCA 699
86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
700 AAAGCCTCCAAATGGATGTCTTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 759
106 IleAlaIleAlaTyIleMetLysArgMetAspMetSerLeuAspGluAlaTyArgPhe 125
760 ATCGCTATCGCTACATCATCATGAAGAGGATGGACATGTCTTTAGATCAAGCTTACAGATTT 819
126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyClnLeuLeuAsp 145
820 GTGAAGAAAGAAAGACCTACTATATCTCCAAATCTTCAATTTCTGGGCCAATCTCTGGAC 879
146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
880 TATGAGAGAGAGATTAGAACACAGACTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTG 939
166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyLysSer 185
940 CTGCACTGGAGAGCAAAATGAACCTGTCTCTGCTGTCTCAGAGGGTGCACAGAAAGC 999
186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaIleGlyGlnArg 205
1000 GAGACGCCCTCAGTCCACCTGTGCCGACTCTGCTTACCTCAGAGCAGCAGCAAGAG 1059
206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
1060 CCGGTGCATCCCGCCAGCGTGCAGCGTCCAGCGTGCAGCGTGCAGCGTGCAGCGAC 1119
226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
1120 AGCCCGCTGTGACAGCGCTCAGTGGCTGCACCTGTCCGACAGCAGGCTGGAGACAGC 1179
246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
1180 AATAAGCTCAAGGTTCTCTCTCTGGATATCAATCAGTTTCATATTTTCAGCCAGCATG 1239
266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyTyLysProSer 285
1240 GCAGCATCTCTACATGGCTTCTCTCATCAGAGATGCTTTGGAACTACTACAACTCTCC 1299
286 ThrThrLeuAspGlyThrAnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
1300 ACTACTCTGGATGGGACCAACAGCTATGCCAGTCTCTCCCTGTTCAGGAATCTCGAG 1359
306 GlnThrProGluThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThr 325
1360 CAGACTCCCGNAACAGTCTCTGTATAGGAGGAGCCAGCATCCCAAGAGCTGCAGACC 1419
326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerGly 345

Db 1420 GCCAGGCTTCAGACAGCCAGCAGGAGTTCATTCGGTCAGAACCCAGCAGCAGTGGC 1479
Qy 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAnTyr 365
Db 1480 ACCGCCAGAGGTCCCTTTTATCTCCACTGTCATCGAAGTGGGAGCGTGGAGGCAATTAC 1539
Qy 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db 1540 CACACCAGCTTCCTTTTGGGCTTTTCCACAGCCAGCAGCACCTCACGAAGTCTGCTGGC 1599
Qy 386 LeuGlyLeuLysGlyTyPheHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db 1600 CTGGCCCTTAAGGGCTGGCATTCGGATATCTTTGGCCCCCAGACCTTACCCCTTCCCTG 1659
Qy 406 ThrSerSerTyrTyPheAlaThrGluSerSerHisPheTySerAlaSerAlaIleTyr 425
Db 1660 ACCAGCAGCTGGTATTTTGGCCACAGAGTCTCTCACATTTCTACTCTGCTCAGCCATCTAC 1719
Qy 426 GlyGlySerAlaSerTyrSerAlaTySerCysSerGlnLeuProThrCysGlyAspGln 445
Db 1720 GGAGCAGTGGCAGTTACTCTGCTTACAGTTCAGCAGCCAGCTGCCACCTTGGGAGACCAA 1779
Qy 446 ValTySerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
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Qy 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
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Qy 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
Db 1900 GAGAGCATCATGTACAGACACAGGTTCACGGGAAGAGCTGGGGAAGTGGCGAGTCACTCT 1959
Qy 506 SerPheSerGlySerMetGluIleIleGluValSer 517
Db 1960 AGCTTTTCGGGCGAGCATGGAATCATTTGAGGTCTCC 1995

RESULT 3

US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US20040009501A1
; GENERAL INFORMATION:
; APPLICANT: Millemium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MPI03-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508

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; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:
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Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 16 Gaps: 1

US-09-964-277-21 (1-517) x US-10-377-072-27 (1-1998)
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DB 281 ATGTTCCTCTCTCTCTCAGACTGTTTCTCAGTGTACTTCTGGGTAACCTGGAGAAGA 340
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
DB 341 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTGTCTGAGTTCCTCTGTTGTTCCCT 399
QY 29 ----- 29
DB 400 GGCCCTCTGTGAAGAAATCCACTAGTCCCTACCTGCAATTTCTCAGCCTTGTTCACCT 459
QY 29 ----- 29
DB 460 GTTGCCCAACATGGGGCAACCCGAATCTTCCCAATCTTTATCTTGCTGGCTGCCAGCAGAT 519
QY 30 -----GlutLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
DB 520 GTCCCTCAACAGGAGCTGATGCAGCAGATGGATGGATGGTATGTTATGTTAATGCCAGCAAT 579
QY 46 ThrCysProLysProAspPheLeuProGluSerHisPheLeuArgValProValAsnAsp 65
DB 580 ACTGTGTCAAAGCCTGACTTATATCCCGAGTCTCATTTCTCGGTGTGCTGTGAATGAC 639
QY 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
DB 640 AGCTTTTGTGAGAAATTTTGGCGTGGTTGGCAAAATCAGTAGATTTCTATTGAGAAAGCA 699
QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
DB 700 AAGCCCTCCAAATGGATGTTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 759
QY 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
DB 760 ATCGCTATCGCCTACATCATGAAGAGATGGACATGCTCTTTAGATGAAGCTTACAGATT 819
QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
DB 820 GTGAAGAAAAAGACCTACTATATCTCCAAACTTTCAATTTTCTGGGGCAACTCCCTGGAC 879
QY 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
DB 880 TATGAGAAGAAATTAAGAACCCAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTG 939
QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185
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DB 940 CTGCACCTGGAGAACCCAAATGAACCTGTCTCTGCTGTCTCAGAGGGTGGACAGAAAAGC 999
QY 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyClnArg 205
DB 1000 GAGAGCCCTTCAGTCCACCTCTGTCGCACTCTGCTACTCAGAGGCGAGGCAAAAGG 1059
QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuGluAsp 225
DB 1060 CCCGTGCATCCCGCAGCGTCCCGAGCTGCCAGCTGCCAGCTGCTCTGTGAGGAC 1119
QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
DB 1120 AGCCCGCTGGTACAGCGCTCAGTGGCTGCACCTGTCCGCGAGACAGCTGGAGACAGC 1179
QY 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
DB 1180 AATAAGCTCAAGCGTTCTCTCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATG 1239
QY 266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
DB 1240 GCAGCATCTTACATGGCTTCTCTCATCAGAGATGCTTTGGGAATACTACAAACCTTCC 1299
QY 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
DB 1300 ACTACTCTGGATGGAGCCACAGCTATGCCAGTTCTCCCTGTTTCAGAACTATCGGAG 1359
QY 306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
DB 1360 CAGACTCCCGAAACCCAGTCTCTGATAAGGAGGAGCAGCAGCTCCCAAGAGCTCAGAGC 1419
QY 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
DB 1420 GCCAGGCTTTCAGACAGCAGCAAGCGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1479
QY 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
DB 1480 ACCGCCACAGAGTCCCTTTTATCTCCACTGCTGATCGAAGTGGAGCGTGGAGACAAATAC 1539
QY 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
DB 1540 CACACCAGCTTCTTTTCGGCTTTCCACCAGCAGCAGCAGCAGCTCAGAGCTCTGCTGG 1599
QY 386 LeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
DB 1600 CTGGGCTTAAAGGCTGGCACTCGATATCTTGGCCCTTGGCCCTCCAGAGCTCTACCCCTTCC 1659
QY 406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
DB 1660 ACCAGCAGCTGTGATTTTGGCAGAGAGTCTCAGACTTCTACTCTGCTCAGCAGCTCTAC 1719
QY 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
DB 1720 GGAGCAGTGGCAGTACTTCTGCTTACAGCTGCGAGCAGCTGCGCCACTTGGGAGACCA 1779
QY 446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
DB 1780 GTCTATTCTGTGCGCAGCGGCGAGCCAGTGCAGAGCTGACTCGCGCGGAGCTGG 1839
QY 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
DB 1840 CATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGCGAGAGCTGCCAAATGGAATTTGGA 1899
QY 486 GluSerIleMetSerGluAsnArgSerArgGluLeuGlyLysValGlySerGluSer 505
DB 1900 GAGAGCATCATGTGAGAGACAGGTCCGGGAAGAGCTGGGGAAGTGGGGAGTGGGCGAGTCT 1959
QY 506 SerPheSerGlySerMetGluIleIleGluValSer 517
DB 1960 AGCTTTTCGGCGCAGCATGGAAATCATTTGAGGTCTCC 1995
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RESULT 4
US-10-377-072-27
Sequence 27 Application US/10377072

QY	386	LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu	405
DB	1600	CTGGGCTTAAGGGCTGGCACTGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG	1659
QY	406	ThrSerSerTrpTrpPheAlaThrGluSerSerHisPheTrpSerAlaSerAlaIleTrp	425
DB	1660	ACCAGCAGCTGGATTTTGGCCACAGAGTCTCTACACTTCTACTCTGCCCTCAGCCATCTAC	1719
QY	426	GlyGlySerAlaSerTrpSerAlaTrpSerCysSerGlnLeuProThrCysGlyAspGln	445
DB	1720	GGAGGCGAGTGGCAGTTACTCTGCTACAGCTGCAGCCAGCTGCCACTTGGGAGACCAA	1779
QY	446	ValTrpSerValArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp	465
DB	1780	GTCTATTCTGTGGCAGCGCGCAGAGCCAAAGTGCAGAGCTGACTCGCGCGGAGCTGG	1839
QY	466	HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly	485
DB	1840	CATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGCAGAGAGCTGCCAAATGGAAATTGGA	1899
QY	486	GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer	505
DB	1900	GAGAGCTCATGTTCAGAGAACAGCTCACGGGAGAGCTGGGGAAGTGGGCGAGTCAGTCT	1959
QY	506	SerPheSerGlySerMetGluIleIleGluValSer	517
DB	1960	AGCTTTTGGGCGAGCATGGAATCATTTAGGTCTCC	1995
RESULT 5			
US-10-094-749-673			
; Sequence 673, Application US/10094749			
; Publication No. US20030219741A1			
; GENERAL INFORMATION:			
; APPLICANT: ISOGAL, TAKAO			
; APPLICANT: SUGIYAMA, TOMOYASU			
; APPLICANT: OTSUKI, TETSUJI			
; APPLICANT: WAKAMATSU, AI			
; APPLICANT: SATO, HIROYUKI			
; APPLICANT: ISHII, SHIZUKO			
; APPLICANT: YAMAMOTO, JUN-ICHI			
; APPLICANT: ISONO, YUUKO			
; APPLICANT: HIO, YURI			
; APPLICANT: OTSUKA, KAORU			
; APPLICANT: NAGAI, KEIICHI			
; APPLICANT: IRIE, RYOTARO			
; APPLICANT: TAMECHIKA, ICHIRO			
; APPLICANT: SEKI, NAOHICO			
; APPLICANT: YOSHIKAWA, TSUTOMU			
; APPLICANT: OTSUKA, MOTOTYUKI			
; APPLICANT: NAGAHARI, KENJI			
; APPLICANT: MASUHO, YASUHIKO			
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA			
; FILE REFERENCE: 084335/0160			
; CURRENT APPLICATION NUMBER: US/10/094,749			
; PRIOR FILING DATE: 2002-03-12			
; PRIOR APPLICATION NUMBER: 60/350,435			
; PRIOR FILING DATE: 2002-01-24			
; PRIOR APPLICATION NUMBER: JP 2001-328381			
; PRIOR FILING DATE: 2001-09-14			
; NUMBER OF SEQ ID NOS: 3381			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 673			
; LENGTH: 2102			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-094-749-673			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Percent Identity:			
Percent Conservation:			
Length:			
Matches:			
Conservative:			
Gap:			
Mismatch:			
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286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
 1355 ACTACTCTGGATGGGACCAACAGCTATGCCAGTTCTCCCTGTTCAGGAACATATCGGAG 1414
 306 GlnThrProGluThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThr 325
 1415 CAGACTCCGGAACCACTCTCTGATAAGAGGAGCCAGCATCCCAAGAGCTGCAGACT 1474
 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerGly 345
 1475 GCCAGGCTTCAGACAGCCAGAGCAAGCATTCGATTCGGTCCAGAACCCAGCAGCTGGC 1534
 346 ThrAlaGlnArgSerLeuSerProLeuHisArgSerGlySerValGluAspAsnThr 365
 1535 ACCGCCAGAGGTCCTTTTATCTCCACTGCATCGAAGTGGAGCGGTGGAGGCAATTAC 1594
 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnHisLeuThrLysSerAlaGly 385
 1595 CACACAGCTTCCTTTTGGCCCTTCACAGCCAGCAGCAGCCTCCAGAGTCTGCTGGC 1654
 386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
 1655 CTGGCCCTTAAGGGCTGGCACTCGGATATCTTGCCGCCCCAGACCTCTACCCCTTCCCTG 1714
 406 ThrSerSerTrpThrPheAlaThrGluSerSerHisPheThrSerAlaSerAlaIleThr 425
 1715 ACCAGAGCTGGTATTTTGGCACAGAGTCTCTACACTTCTACTCTGCCCTCAGCCATCTAC 1774
 426 GlyGlySerAlaSerTrpSerAlaThrSerCysSerGlnLeuProThrCysGlyAspGln 445
 1775 GGAGCAGTCCAGTACTTCTGCTACAGCTGCAGCCAGCTGCCCTTGGGAGACCAA 1834
 446 ValTrpSerValArgArgAsgLysProSerAspArgAlaAspSerArgArgSerTrp 465
 1835 GTCTATTCTGTGGCAGCGCGCAGAGCCAAAGTGACAGAGCTGACTCGCGCGGAGCTGG 1894
 466 HisGluLeuSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
 1895 CATGAAGAGAGCCCTTTGTGAAAAGCAGTTTAAACGCCAGAGAGCTGCCAAATGGAAATTGGA 1954
 486 GluSerIleMetSerGluAsnArgSerArgGluLeuLysValGlySerGlnSer 505
 1955 GAGAGCATCATGTACAGACAGAGTACAGGAGAGAGCTGGGAAAGTGGCAGTCACTCT 2014
 506 SerPheSerGlySerMetGluIleLeuGluValSer 517
 2015 AGCTTTTCGGGAGCATGGAAATCATTGAGGTCTCC 2050

ESULT 6

S-10-168-506-2

Sequence 2, Application US/10168506

Publication No. US20040053229A1

GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY D.

APPLICANT: MARTINEZ, RICARDO

APPLICANT: WHYTE, DAVID

APPLICANT: MANNING, GERARD

APPLICANT: SUDARSANAM, SUCHA

APPLICANT: HILL, RON

APPLICANT: FLANAGAN, PETER

TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES

FILE REFERENCE: 038602/1351

CURRENT APPLICATION NUMBER: US/10/168,506

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: PCT/US00/34736

PRIOR FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 2732

TYPE: DNA

ORGANISM: Homo sapiens

S-10-168-506-2

Alignment Scores:

Pred. No.: 9,82e-260 Length: 2732

Score: 2606.00 Matches: 516

Percent Similarity: 90.21% Conservative: 0

Best Local Similarity: 90.21% Mismatches: 1

Query Match: 97.68% Indels: 56

DB: 13 Gaps: 1

US-09-964-277-21 (1-517) x US-10-168-506-2 (1-2732)

QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
 DB 818 ATGTGTGCTCTCTCTCTTCAGACGTGTTTCTCACTGACTTCTGGGTAAACTGGAGAAGA 877
 QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
 DB 878 GCTTCAACTCTGTTCACTGCTTGA- GGTGGGTTTGTGAGTTCTCTCGTTGTTTCCCT 936
 QY 29 ----- 29
 DB 937 GGCCTCTGTGAAGGAAAAATCCACTCTAGTCCCTACCTGCATTTCTCGACCTTGTCTTACCT 996
 QY 29 ----- 29
 DB 997 GTTGCCAACTTTGGGCCNAACCCGAAATTTCTCCCAATCTTTATCTTGGTGGCCAGCGAGAT 1056
 QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
 DB 1057 GTCTTCAACAGGAGCTGATGCAGCAGAAATGGGATGTTATGTATGTATGTTAAATGCCAGCAAT 1116
 QY 46 ThrCysProLysProAspPheIleProGlnSerHisPheLeuArgValProValAsnAsp 65
 DB 1117 ACCTGTCCAAAGCCCTGACTTTATCCCGAGTCTCATTTCTCGCGTGTGCTGTGAATGAC 1176
 QY 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
 DB 1177 AGCTTTTGTGAGAAAATTTTGGCGGTGGACAAATCAGTAGAATTTCAATTGAGAAAGCA 1236
 QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
 DB 1237 AAAGCTTCAATGATGTTCTTAGTCACCTGTTTAGTGGATCTCCCGCTCCGCCACC 1296
 QY 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
 DB 1297 ATCGCTATCGCTACATCATGAGAGGATGGACATGCTTTTAGATGAAGCTTACAGATT 1356
 QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlnLeuLeuAsp 145
 DB 1357 GTGAAAGAAAAGAACCTTACTATATCTCCAACTTCAATTTTCTGGGCCAACTCCTCTGCAC 1416
 QY 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
 DB 1417 TATGAGAGAGATTTAGAACACAGCTGGACATCAGGCCCAAGAGCAAACTCAAGCTG 1476
 QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185
 DB 1477 CTGCACCTGGAGAGGCCAAATGAACCTGTCTCTCAGAGGGTGGACAGAAAGC 1536
 QY 186 GluThrProLeuSerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
 DB 1537 GAGAGCCCTTCACTGTCACCTGTGCGGACTCTCTACCTCAGAGGCGAGGCAAGG 1596
 QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
 DB 1597 CCGTGTATCCCGCAGCGTCCAGCGTGGCCAGCGTGGCCGCTGCTGCTGTTAGAGGAC 1656
 QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
 DB 1657 AGCCCGCTGTGTACAGGGGCTCAGTGGGCTGCACCTGTCCGAGACAGGCTGGAGAGACAGC 1716
 QY 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265

1142 AGCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCGACACAGAGGCTGGAGACAGC 1201
246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerAlaSerMet 265
1202 AATAAGCTCAAGCGTCTCTCTCTGGATCAAAATCAATTCATATTCAGGACAGCATG 1261
266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
1262 GCAGCATCTTACATGGCTTCTCTCTACAGAGATGCTTTGGAAATACATCAAACTTCC 1321
286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
1322 ACTACTCTGATGGAGCAACCAAGCATGATCCAGTTCTCCCTCTGTTCCAGGAATATCGGAG 1381
306 GlnThrProGlnThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThr 325
1382 CAGACTCCGAAACAGTCTCTGTAAGAGAGAGAGCCAGCATCCCAAGAGTGCAGACC 1441
326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
1442 GCCAGGCTTTCAGACACAGCAGACGAGATGATTCGTTGATGAGACAGCAGATGGC 1501
346 ThrAlaGlnArgSerLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
1502 ACCGCCAGAGGTCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGCAATTAC 1561
366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnHisLeuThrLysSerAlaGly 385
1562 CACACAGCTTCTCTTTTGGGCTTTTCCAGCAGCAGCAGCAGCAGCAGTCTGCTGGC 1621
386 LeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
1622 CTGGGCTTTAAGGCTGGGCTGGACTCGATATCTTGCCCCCAGACCTTACCCCTTCCCTG 1681
406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
1682 ACCAGCAGCTGGTATTTTGGCCAGAGAGTCTCACACTTCTACTCTGCTCAGCCATCTAC 1741
426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
1742 CGAGCAGTGCAGTACTCTGCTACAGCTGAGCAGCAGCAGCAGCAGTGGGAGACCAA 1801
446 ValTyrSerValArgAGATGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
1802 GTCTATTCTGTGCGCAGCGGAGAGCCAGAGTAAAGCAGCTTTAAAGCAGAGCTGCCAATGGAATTGGA 1861
466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
1862 CATGAACAGAGCCCTTTTGAAGAGCAGTTTAAAGCAGAGCTGCCAATGGAATTGGA 1921
486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
1922 GAGAGCATCATGTGAGAGAACAGGTACCGGAGAGAGTGGGAGAGTGGGAGTCACTGCT 1981
506 SerPheSerGlySerMetGluIleLeuValSer 517
1982 AGCTTTTGGGCGCATGGAAATCATTTGAGGTCTCC 2017

RESULT 8

S-10-257-026-1

Sequence 1, Application US/10257026

Publication No. US2004008659A1

GENERAL INFORMATION:

APPLICANT: Merck Patent GmbH

TITLE OF INVENTION: New dual specificity phosphatase

FILE REFERENCE: DUSP10K0WS

CURRENT APPLICATION NUMBER: US/10/257,026

CURRENT FILING DATE: 2003-11-07

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 3059

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (127)..(2121)
US-10-257-026-1

Alignment Scores:

Pred. No.: 1,16e-259 Length: 3059
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 1 Gaps: 1

US-09-964-277-21 (1-517) x US-10-257-026-1 (1-3059)

QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArg 20
Db 407 ATGTGCTCTCTCTCTCTCAGACGTTTCTCACTGTACTTCTGGTAAACTGCGAGA 466
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
Db 467 GCTTCAACTCTGTTCACCTGCTTGCA-GGTGGGTTTGTGAGTTCTCTCGTTGTTCCCT 525
QY 29 ----- 29
Db 526 GGCCTCTGTGAAGGAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTGTGTTACCT 585
QY 29 ----- 29
Db 586 GTTCCACATTTGGGCAACCCGAAATCTTCCCAATCTTATCTTGGCTGCCAGGAGAT 645
QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db 646 GTCTCTCAACAGGAGCTGATGCAGAGAATGGGATTGGTTATGTGTAAATGCCAGCAAT 705
QY 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
Db 706 ACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCTCGGTGGCTGTGATGAC 765
QY 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
Db 766 AGCTTTTGTGAGAAATTTTGGCGTGGTGGACAAATCAGTAGATTTTCAATGAGAAAGCA 825
QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db 826 AAAGCCTCCAATGGATGTGTTCTAGTGCACCTGTTTAGCTGGGATCTCCCGCTCCGCCACC 885
QY 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db 886 ATCGCTATCGCTACATCATGAGAGGATGACATGCTTTTAGATGAAGCTTACAGATTT 945
QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db 946 GTGAAGAAAGAAAGACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCGAC 1005
QY 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
Db 1006 TATGAGAAGAGATTAAAGAACCCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1065
QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185
Db 1066 CTGACCTTGGAGAAGCCAAATGAACCTGTCTCTGCTCTCAGAGGGTGGACAGAAAGC 1125
QY 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db 1126 GAGAGCCCTCAGTCCACCTGTGGCCGACTCTGCTACCTCAGAGGCGAGCAGCAAGG 1185
QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db 1186 CCCGTGATCCCGCAGCGTGCAGCCAGCGTGCAGCGCGTGCAGCGCTGCTGTTAGAGGAC 1245

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QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
DB 1246 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCGACAGACAGCTGGAGACAGC 1305

QY 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
DB 1306 AATAAGCTCAAGCGCTCTCTCTCTGATATCAATCAGTTTCATATTCAGCCAGCATG 1365

QY 266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
DB 1366 GCAGATCCTTACATGCTTCTCTCTCAAGAGATGCTTTGGAATACTCAACACCTTCC 1425

QY 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
DB 1426 ACTACTCTGATGGGACCAACAGCTATGCGAGTCTCTCCCTGTTCAAGGAACATTCGAG 1485

QY 306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
DB 1486 CAGACTCCCGAAACAGCTCTGATAAGGAGCAAGCCAGCATCCCAAGAGCTGAGACC 1545

QY 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerGly 345
DB 1546 GCAGGCGCTTCACAGACCCAGCAAGCGATTGCTTCGCTCAGAACCCAGCAGCAGTGGC 1605

QY 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
DB 1606 ACCGCCAGAGGTCCTTTTATCTCAGCTGCAAGTGGAGCGTGGAGACAAATTAC 1665

QY 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnHisLeuThrLysSerAlaGly 385
DB 1666 CACACAGCTTCTCTTTCGCGCTTTCACACGAGCAGCAGCAGCTCAGCAAGTCTGCTGGC 1725

QY 386 LeuGlyLeuLysGlyThrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
DB 1726 CTGGGCGCTTAAGGCGTGGCACTCGGATATCTTGGCGCCCGACAGCTCTACCCCTTCCCTG 1785

QY 406 ThrSerSerThrTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
DB 1786 ACCAGCAGCTGGTATTTTGGCACAGAGTCTCTCACACTTCTACTCTGCTCAGCCATCTAC 1845

QY 426 GlyLysAlaSerTyrSerAlaTyrSerCysSerGlnLeuProGlnThrSerThrCysGlyAspGln 445
DB 1846 GGAGGAGTGGCCAGTACTCTGCTTACAGTCCAGCCAGCTGAGCTGCTGCGGCGAGCTGG 1905

QY 446 ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTyr 465
DB 1906 GTCTATCTGTCGCGAGCGGCGAGCAAGCCAGTGCAGCTGAGCTGCTGCGGCGAGCTGG 1965

QY 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
DB 1966 CATGAAGAGAGCGCCCTTTTGAAGAAGCAGTTTAAACGCAAGAGTGCCTGCAATTTGGA 2025

QY 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
DB 2026 GAGAGCATCATGTCAAGAACAGGTGTCGCGGAGAGCTGGGGAAAGTGGCGAGTCACTCT 2085

QY 506 SerPheSerGlySerMetGluIleLeuGluValSer 517
DB 2086 AGCTTTTCGGGCGAGCATGGAAATCATTCAGGTCTCC 2121

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RESULT 9

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US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

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Alignment Scores:

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Pred. No.: 1,41e-259 Length: 3496
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 9 Gaps: 1

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US-09-964-277-21 (1-517) x US-09-964-277-1 (1-3496)

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QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTyrValAsnTyrArgArg 20
DB 842 ATGTTGCCCTCTCTCTCTCAGACTGTTTCTCAGCTGTACTTCTGGGTAAACTGGGAGAAGA 901

QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
DB 902 GCTTCAACTCTGTTTCCACTGCTTGA-GGTGGGTTTGGTGGAGTCTCTCGTTGTTTCCCT 960

QY 29 ----- 29
DB 961 GGCCTCTGTGAAGGAAATCCACTCTAGTCCCTAGCTTCTCAGCCTTGTCTTACCT 1020

QY 29 ----- 29
DB 1021 GTTCCAACTTGGGCCCAACCCGAAATCTTCCCAATCTTATCTTGGCTGCCAGCAGAT 1080

QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
DB 1081 GTCCTCAACAGAGAGCTGATCGACAGAAATGGGATTTGTTATGTTTAAATGCCAGCAAT 1140

QY 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
DB 1141 ACCTGTCCAAAGCTGACTTTATCCCGAGTCTCATTTCTGCTGCTGCTGCTGCTGCTGCTG 1200

QY 66 SerPheCysGluLysIleLeuProTyrLeuAspLysSerValAspPheIleGluLysAla 85
DB 1201 AGCTTTTGTGAGAAAATTTTCCCGTGGTGGACAAATCAGTAGATTTTCATTGAGAAAGCA 1260

QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
DB 1261 AAGCTTCCCAATGATGTTCTAGTGCATGTTTGTAGTGGATCTCCGCTCCGCCACC 1320

QY 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
DB 1321 ATCGTATCGCTACATCATGAGAGATGGAATGTCATGTTTGTAGTGAAGCTTACAGATT 1380

QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
DB 1381 GTGAAGAAAAGAGACCTACTATATCTCCAACTTCAATTTTCTGGGCCCAACTCTCGGAC 1440

QY 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
DB 1441 TATGAGAAAGAGATTAAAGAACCCAGACTGGAGCATCAGGGCCAAAGAGCAACTCAAGCTG 1500

QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185
DB 1501 CTGCCTCTGAGAGCCAAATGAACCTGTCCTCTGCTGCTCTCAGAGGGTGGACAGAAAGC 1560

QY 186 GluThrProLeuSerProCysAlaAspSerAlaThrSerGluAlaIleGlyGlnArg 205
DB 1561 GAGAGCGCCCTCAGTCCACCTGTCGCGACTCTGCTACTCTCAGAGGCGAGGAGCAAGAG 1620

QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
DB 1621 CCGTGCATCCGCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCG 1680

QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245

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> 1681 AGCCGCTGGTACAGCGCTCAGTGGCTGCACCTCTCCGACAGACAGCTGGAGACAGC 1740
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/ 246 AsnLysLeuLysArgSerPheSerLeuAspLleLysSerValSerTyrSerAlaSerMet 265
/
/ 1741 AATAAGCTCAAGCGTCTCTCTCTGATCAATCAATCAGTTTCATATTCAGCCAGCATG 1800
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/ 266 AlaAlaSerLeuHisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
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/ 1801 GCAGATCCTTACATGGCTCTCTCTCATCAGAGATGCTTTGGAATACTACAACCTTCC 1860
/
/ 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
/
/ 1861 ACTACTCTGGATGGACCAACAAGCTATGCCAGTTCTCCCTCTGTTCCAGAACTATCGGAG 1920
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/ 306 GlnThrProGluThrSerProAspLysGluLalaSerLleProLysLysLeuGlnThr 325
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/ 1921 CAGACTCCCGAAACAGTCTCTGATTAAGAGAAAGCCAGCATCCCAAGAAAGTGCAGACC 1980
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/ 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
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/ 1981 GCCAGGCTTCAGACAGCCAGCAACCGAATGCAATTCGGTTCAGAACCCAGCAGCTGGC 2040
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/ 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
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/ 2041 ACCGCCAGAGTCCCTTTTATCTCCACTGCNTCGAAGTGGAGCGTGGAGGACAATTAC 2100
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/ 2101 CACACAGCTTCTCTTTTCCGCTTTCACAGCAGCAGCAGCAGCAGCAGTCTGCTGGC 2160
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/ 386 LeuGlyLeuLysGlyTyrHisSerAspLleLeuAlaProGlnThrSerThrProSerLeu 405
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/ 2161 CTGGGCTTTAAGGCTGGCACTGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG 2220
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/ 406 ThrSerSerTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaLleTyr 425
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/ 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
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/ 2281 GGAGCAGTGCAGTTACTCTGCTACAGCTCAGCAGCAGCTGCCCCACTTGGGAGACCAA 2340
/
/ 446 ValTyrSerValArgArgGlnLysProSerAspAlaAspSerArgArgSerTyr 465
/
/ 2341 GTCTATTCTGTGGCCAGCGCCAGAGCCAAAGTGCAGAGCTGACTCGCGCGAGCTGG 2400
/
/ 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
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/ 2401 CATGAAGAGAGCCCTTTGAAGACAGTTTAAACGAGAGCTGCCAAATGGAAATTGGA 2460
/
/ 486 GluSerIleMetSerGluAsnArgSerArgGlnGluLeuGlyLysValGlySerGlnSer 505
/
/ 2461 CAGAGCATCATGTCCAGAAACAGGTACCGGAGAGCTGGGAAAGTGGGCACTCAGTCT 2520
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/ 506 SerPheSerGlySerMetGluIleLeuValSer 517
/
/ 2521 AGCTTTTGGGCGACATGGAAATCATTTGGGTCTCC 2556

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RESULT 10

US-09-816-494-1

Sequence 1, Application US/09816494

Patent No. US20020034807A1

GENERAL INFORMATION:

APPLICANT: Meyers, Rachel A.

TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY

TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR

FILE INVENTION: 10448-030002

CURRENT APPLICATION NUMBER: US/09/816,494

PRIOR FILING DATE: 2001-03-23

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3544

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (589)....(2583)

US-09-816-494-1

Alignment Scores:

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Pred. No.: 1,446-259 Length: 3544
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 9 Gaps: 1

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US-09-964-277-21 (1-517) x US-09-816-494-1 (1-3544)

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DB 869 ATGTTGGCTCTCTCTCTTTCAGACTGTTTCTCACTACTCTCTGGTAAATCGGAGAAGA 928
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
DB 929 GCTTCAACTCTGTTCACTGCTTGA--GGTGGTTGCTGAGTTCTCTCGTTGTTTCCT 987
QY 29 ----- 29
DB 988 GSCCTCTGTGAAGGAAATCACTCTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCT 1047
QY 29 ----- 29
DB 1048 GTTGCCAACTTTGGGCCAACCCGAAATCTTCCCAATCTTTATCTTGGCTGCCAGCAGAT 1107
QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
DB 1108 GTCCTCAACAGAGAGCTGATCGACAGAAATGGAAATGGTTAATGTTAATGCCAGCAAT 1167
QY 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
DB 1168 ACCTGTCCAAAGCCTGACTTTATCCCGAGTCTCATTTCTCGGTGCTGCTGCAATGAC 1227
QY 66 SerPheCysGluLysLleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
DB 1228 AGCTTTTGTGAGAAAATTTTCCCGTGGTGGACAAATCAGTAGATTTTCATTGAGAAAGCA 1287
QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
DB 1288 AAAGCTCCAAATGGATGTTTCTAGTGCATGTTTAGCTGGATCTCCCGTCCGCCACC 1347
QY 106 IleAlaLleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
DB 1348 ATCGCTATCGCTACATCATCAAGAGGATGACATGCTTTTAGTAGAAGCTTCAGATTT 1407
QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuAsp 145
DB 1408 GTGAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCGCAACTCTCTGAC 1467
QY 146 TyrGluLysLysLleLysAsnGlnThrGlyAlaSerGlyProLysSerLeuLysLeu 165
DB 1468 TATGAGAAGAAAGATTAGAACCCAGACTGGAGCATCAGGCGCCAAAGAGCAAACTCAAGCTG 1527
QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
DB 1528 CTGCACCTGGAGAAAGCAAAATGAACCTGTCTCTCAGAGGTGGACAGAAAGC 1587
QY 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
DB 1588 GAGACGCCCTCAGTCCACCTGTGCGCACTCTGTACTCTCAGAGGCGCAGCAGCAAGG 1647
QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuAsp 225

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1168 ACCTGTCCAAAGCCCTGACTTTATCCCGAGTCTCATTTCTCGGTGCTGTGAATGAC 1227
66 SerPheCysGluLysLeuProThrLeuAspLysSerValAspPheIleGluLysAla 85
1228 AGCTTTTGTGAGAAATTTTGGCGGTGGTGGCAAAATCAGTAGATTTTCAATGAGAAAGCA 1287
86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
1288 AAAGCTCCATGGATGTGTCTAGTGCATCTTTAGTGTGGATCTCCCGCTCCGCCACC 1347
106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
1348 ATCGCTATCGCTACATCATGAGAGGATGGACATGTCTTTAGATGAAGCTTTACAGATTT 1407
126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
1408 GTGAAGAAAAAGACCTACTATATCTCCAAATCTCAATTTTCTGGGCCAACTCTCTGGAC 1467
146 TyrGluLysLeuIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
1468 TATGAGAAGAGATTAAAGAACAGACTGGAGCATCAGGCCAAGAGCAAACTCAAGCTG 1527
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1528 CTGCACCTGGAGAGCAAAATGAACCTGTCTCTGTCTCAGAGGGTGGACAGAAAGC 1587
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1588 GAGAGCCCTCAGTCCACCTGTGCGGACTCTGTCTACCTCAGAGGACAGCAGCAAAAG 1647
206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
1648 CCGCTGCATCCCGCCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGC 1707
226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
1708 AGCCCGCTGGTACAGCGCTCAGTGGGCTGCACCTGTCCGACAGCGCTGGAAGACGC 1767
246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerThrSerAlaSerMet 265
1768 ATAAGCTCAGCGTTCCTTCTCTGGATATCAATCAGTTTCATATTTCAGCCAGCATG 1827
266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
1828 GCAGCATCTTACATGGCTTCTCTCATCAGAAGATGCTTTGGAATCTACAAACCTTCC 1887
286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnLeuLeuSerGlu 305
1888 ACTACTCTGGATGGGACCAACAGCTATGCCATGCTCTCCCTGTTCCAGGAATCTCGGAG 1947
306 GlnThrProGluThrSerProAspLysGluAlaSerIleProLysLysLysLeuGlnThr 325
1948 CAGACTCCCGAAACCCAGTCTCTGATAGGAGGAGCCAGCATCCCCAAGAGCTCCAGACC 2007
326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
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2128 CACACCAAGCTTCTTTTGGCGCTTTCACAGCAGCAGCAGCAGCAGTCTCGAAGTCTGTGGC 2187
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2188 CTGGCGCTTAAGGGCTGGCACTCGATATCTTGGCCCCCAGACCTTACCTCCCTTCCCTG 2247
406 ThrSerSerThrPheAlaThrGluSerSerHisPheThrSerAlaSerAlaIleTyr 425

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2308 GGAGGAGTGGCCAGTACTCTCTGCTACAGCTGCAGCAGCTGCCACTTGGCGAGACCAA 2367
446 ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgSerTrp 465
2368 GTCTATTCTGTGCGCAGCGCCAGAAAGCAAGTGCAGAGCTGACTCCGCGGAGCTGG 2427
466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
2428 CATGAAGAGAGCCCTTTGAAGAGCAGTTTAAACGACAGAGCTGGGGAAGTGGCAGTCT 2487
486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
2488 CAGAGCATCATGTACAGAAAGCTCAGCGGAGAGCTGGGGAAGTGGCAGTCTCAGTCT 2547
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2548 AGCTTTTCCGCGCAGCATGCAATCATTCATTGAGGTCTCC 2583

RESULT 12

US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP103-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2586)
US-10-377-072-25

Alignment Scores:

Pred. No.: 1,446-259 Length: 3544
 Score: 2606.00 Matches: 516
 Percent Similarity: 90.21% Conservative: 0
 Best Local Similarity: 90.21% Mismatches: 1
 Query Match: 97.68% Indels: 56
 DB: 17 Gaps: 1

US-09-964-277-21 (1-517) x US-10-377-072-25 (1-3544)

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 Db 869 ATGTTGCCCTCTCTCTTCAGACTGTTTCTCACTGACTTCTTGGGTAACTGGAGAAGA 928
 Qy 21 AlaSerThrLeuPheThrCysLeuGln----- 29
 Db 929 GCTTCAACTGTTTCACTGCTTGCATGCA-GGTGGGTTTGTCTGAGTTCTCTGTTGTTCCCT 987
 Qy 29 ----- 29
 Db 988 GGCTCTGTGAAGAAATCCACTAGTCCCTACCTGCAATTTCTCAGCCTTTGCTTACCT 1047
 Qy 29 ----- 29
 Db 1048 GTTGGCAACATTTGGGCAACCCGAATCTTCCCATCTTTATCTTGGCTGGCAGAGAT 1107
 Qy 30 -----GlutLeuMetGlnGlnAsnGlyLeGlyTyrValLeuAsnAlaSerAsn 45
 Db 1108 GTCTTCAACAAAGAGCTGATGTCAGCAGAAATGGATGGTATGCTTTAATGCCAGCAAT 1167
 Qy 46 ThrCysProLysProAspPheLeProGluSerHisPheLeuArgValProValAsnAsp 65
 Db 1168 ACCTGTCCAAAGCCTGACTTATPCCCGAGTCTCATTTCTGCTGTGCTGTGAATGAC 1227
 Qy 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
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 Db 1288 AAAGCTCCAAATGATGTGTTCTAGTGCCTGTTTGTAGCTGGATCTCCCGCTCCCGCAC 1347
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 Db 1348 ATCGCTATCGCTTACATCATGAAGAGATGGACATGCTTTTAGATGAAGCTTACAGATT 1407
 Qy 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
 Db 1408 GTGAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCCACTCTCTGGAC 1467
 Qy 146 TyrGluLysValIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
 Db 1468 TATGAGAAAGATTAAGAACCCAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTG 1527
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 Db 1528 CTGGACCTGGAGAGCAATGACCTGCTCTCTGCTGCTCAGAGGGTGGCAGAGAAAGC 1587
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 Db 1588 GAGAGCGCCCTCAGTCCACCTGTGCGGACTCTGCTACCTCAGAGCGAGCAGCAAAAGG 1647
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 Db 1648 CCCGTGCAATCCCGCAGCGTGCACCGTGCACCGTGCACCGTGCACCGTGCCTGTGTAGAGAC 1707
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 Db 1708 AGCCGCTGTTACAGGCGCTCAGTGGGCTGACCTGTCCGACAGAGCGCTGGAAGACAGC 1767
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 Qy 305 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
 Db 1948 CAGACTCCCGAAACAGTCTCTGATAAGGAGGAGGAGCAGCATCCCAAGAGCTCGAGACC 2007
 Qy 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
 Db 2008 GCCAGGCTTCAGACAGCCAGCAAGCGATTGCATTCCGTCAGAACCCAGCAGCAGTGGC 2067
 Qy 346 ThrAlaGlnArgSerLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
 Db 2068 ACCGCCCAAGAGTCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGCAAAATTAC 2127
 Qy 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
 Db 2128 CACACCAGCTTCTCTTTCGGCTTTCACACAGCAGCAGCAGCCTCACGAGTCTGCTGGC 2187
 Qy 386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
 Db 2188 CTGGGCTTTAAGGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG 2247
 Qy 406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
 Db 2248 ACCAGCAGCTGGTATTTTGGCCACAGAGTCTCTCACACTTCTACTCTGCTCAGCCATCTAC 2307
 Qy 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
 Db 2308 GGAGCAGTGCAGTTACTCTGCTTACAGCTGCAGCAGCAGTGCCTTGGGGAGACCA 2367
 Qy 446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
 Db 2368 GTCTATTCTGTGGCAGGCGCAGAGCCAGTACAGAGTGACTCGCGCGGAGCTGG 2427
 Qy 466 HisGluLysProPheGluLysGlnPheLysArgSerCysGlnMetGluPheGly 485
 Db 2428 CATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGCAGAGAGTCCCAAATGGAATTTGA 2487
 Qy 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuLysValGlySerGlnSer 505
 Db 2488 GAGAGCATCATGTGAGAGAACAGGTACGGGAAGAGCTGGGGAAGTGGGCGAGTCAGTCT 2547
 Qy 506 SerPheSerGlySerMetGluIleLeuValSer 517
 Db 2548 AGCTTTTGGGCGAGCATGGAAATCATTTGAGGTCTTCC 2583

RESULT 13

US-10-425-114-26234
 ; Sequence 26234, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 26234
 ; LENGTH: 3625

TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI

S-10-425-114-26234

Alignment Scores:

red. No.: 1.49e-259 Length: 3625
core: 2606.00 Matches: 516
percent Similarity: 90.21% Conservativeness: 0
best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
B: 13 Gaps: 1

S-09-964-277-21 (1-517) x US-10-425-114-26234 (1-3625)

Y 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheThrValAsnTrpArgArg 20
b 972 ATGTGGCTCTCTCTCTCAGACTGTTTCTCACTGACTTCTGGGTAACTGGAGAAGA 1031
Y 21 AlaSerThrLeuPheThrCysLeuGln----- 29
b 1032 GCTTCAACTCTGTTCACTGCTTGCA- GGTGGGTTGGCTGAGTTCTCTCGTTTCCCT 1090
Y 29 ----- 29
b 1091 GGCCTCTGTGAAGGAAATCCACTCTAGTCCCTACCTGCATTCTCAGCCTTTCCTAACCT 1150
Y 29 ----- 29
b 1151 GTTGCCAACTTGGGCCAACCGCAATCTTCCCAATCTTTATCTGGCTGCCAGCGAGAT 1210
Y 30 -----GluLeuMetGlnGlnAnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
b 1211 GTCTCTCAACAGAGCTGATGAGCAGAGATGGGATGGTTATGTGTAAATGCCAGCAAT 1270
Y 46 ThrCysProLysProAspPheLeuProGluSerHisPheLeuArgValProValAsnAsp 65
b 1271 ACTGTCCAAAGCCTGACATTTATCCCGAGTCTCATTTCTCGGTGCTGTGAATGAC 1330
Y 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
b 1331 AGCTTTTGTGAGAAATTTTTCGGTGTGGCAATCAGTAGATTTTATTGAGAAGCA 1390
Y 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
b 1391 AAAGCCTCCAATGATGTGTTCTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCCACC 1450
Y 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
b 1451 ATCGCTATCGCTTACATCATGAAGAGAGATGGACATGCTCTTTAGATGAAGCTTACAGATT 1510
Y 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
b 1511 GTGAAGAAAGAAAGACTACTATATCTCAACTTCATTTCTTGGGCCCACTCTGGAC 1570
Y 146 TyrGluLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
b 1571 TATCAGAGAAGATTAAAGAACAGACTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTG 1630
Y 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185
b 1631 CTGCACCTCGAGAAGCAAAATGAACCTGTCTCCCTGCTCTCAGAGGGGTGACAGAAAGC 1690
Y 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
b 1691 GAGACCCCTCAGTCCACCTGTGCGGACTCTGCTACCTCAGAGGAGCAGAGCAAAAGG 1750
Y 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
b 1751 CCGGTGCATCCCGCAGGTGCCAGGTGCCAGGTGCCAGGTGCCAGGTGCCAGGTGCCAGGT 1810
Y 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245

Db 1811 AGCCCGCTGGTACAGCGCTCAGTGGCTGCACCTGTCGCGAGCAGGCTGGAACACAGC 1870
Qy AenLysLeuLysArgSerPheSerLeuAspIleLysSerValSerLysSerAlaSerMet 265
Db 1871 ATAAGCTCAAGCGTTCTCTCTCTGATATCAATCAGTTTATTCACCCAGCATG 1930
Qy 266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db 1931 GCAGCATCTTACATGGCTTCTCTCATCAGAGATGCTTTGGAATACTTACAAACCTTCC 1990
Qy 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db 1991 ACTACTCTGGATGGGACCAACAGCTATGCCAGTTCTCCCTGTTTCAGAACTATCGGAG 2050
Qy 306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
Db 2051 CAGATCTCCGAAACCGCTCTGATAGAGAGAGGAGCAGCATCCCCAGAGAGCTGAGACC 2110
Qy 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
Db 2111 GCCAGSCCTTCAGACAGCAGCAGCAAGCATTCGATTCGGTCAGAACCCAGCAGCATGTC 2170
Qy 346 ThrAlaGlnArgSerLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db 2171 ACCGCCCAGAGTCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGACAATTAC 2230
Qy 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db 2231 CACACCGCTTCTCTTTTCGGCTTTCACCCAGCAGCAGCCTCACGAAGTCTGCTGGC 2290
Qy 386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db 2291 CTGGSCCTTAAGCGCTGGCATCTCGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG 2350
Qy 406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db 2351 ACCACGAGCTGGTATTTTGGCCACAGAGTCTTCACACTTCTACTCTGCTCAGCCTACTAC 2410
Qy 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db 2411 GGAGCAGTGCCTGCTTACTCTGCTTACAGCTGACAGCTGCTGCCACCTTGGCGGAGACCA 2470
Qy 446 ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
Db 2471 GTCTATTCTGTGCGCAGCGGAGAGCAAGCTTAAACGAGAGCTGACTCGCGCGGAGCTGG 2530
Qy 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db 2531 CATGAGAGAGAGCCCTTTGAAAGCAGTTTAAACGAGAGCTGCCAATGGAATTGGA 2590
Qy 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
Db 2591 GAGAGCATCATGTCAGAGAACAGGTTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCT 2650
Qy 506 SerPheSerGlySerMetGluIleLeuLeuValSer 517
Db 2651 AGCTTTTGGCGCAGCATGGAAATCATTTGAGGTCTCC 2686

RESULT 14

US-10-343-357-17

; Sequence 17, Application US/10343357

; Publication NO. US20040058341A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom

; APPLICANT: ELLIOTT, Vicki S.; RAMKUMAR, Jayalaxmi

; APPLICANT: YAO, Monique G.; BURFORD, Neil

; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.

; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.

; APPLICANT: LEE, Ernestine A.; HAPALIA, April J.A.

; APPLICANT: LU, Dying Aina M.; TRIBOULEY, Catherine M.

; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.

; APPLICANT: YUE, Henry; WARREN, Bridget A.

APPLICANT: NGUYEN, Damiel B.; CHAWLA, Narinder K.
 APPLICANT: KEARNEY, Liam
 TITLE OF INVENTION: PROTEIN PHOSPHATASES
 FILE REFERENCE: PI-0173 PCT
 CURRENT APPLICATION NUMBER: US/10/343,357
 CURRENT FILING DATE: 2003-01-28
 PRIOR APPLICATION NUMBER: PCT/US01/23716
 PRIOR FILING DATE: 2001-07-26
 PRIOR APPLICATION NUMBER: US 60/221,679
 PRIOR FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: US 60/223,272
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: US 60/224,309
 PRIOR FILING DATE: 2000-08-10
 PRIOR APPLICATION NUMBER: US 60/226,728
 PRIOR FILING DATE: 2000-08-18
 PRIOR APPLICATION NUMBER: US 60/229,254
 PRIOR FILING DATE: 2000-08-30
 PRIOR APPLICATION NUMBER: US 60/231,366
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PERL Program
 SEQ ID NO 17
 LENGTH: 3766
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CB1
 US-10-343-357-17

Alignment Scores:

Pred. No.: 1.58e-259 Length: 3766
 Score: 2606.00 Matches: 516
 Percent Similarity: 90.21% Conservative: 0
 Best Local Similarity: 90.21% Mismatches: 1
 Query Match: 97.68% Indels: 56
 DB: 13 Gaps: 1

US-09-964-277-21 (1-517) x US-10-343-357-17 (1-3766)

QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyPheTrpValAsnTrpArgArg 20
 DB 818 ATGTTGCTCTCTCTTCAGACTGTTTCTCAGTCTACTTCTGGGTAACTGGAGAGA 877
 QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
 DB 878 GCTTCAACTCTGTTTCACTGCTGCA-GGTGGGTTTGCTGAGTTCTCTGTTTCCCT 936
 QY 29 ----- 29
 DB 937 GGCCTCTGTGAAGAAAATCCACTCTAGTCCCTACTGCAATTTCTCAGCCTTGCTTACCT 996
 QY 29 ----- 29
 DB 997 GTTGCCACATTTGGGCCAACCCGAATTTCTCCCAATCTTTATCTTGGCTGCCGAGAT 1056
 QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyPheValLeuAsnAlaSerAsn 45
 DB 1057 GTCCTCAACAAGGAGCTGATGCGAGAGAATGGATGGTTATGTGTAAATGCCAGCAAT 1116
 QY 46 ThrCysProValProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
 DB 1117 ACTGTGCAAGGCTGACTTATPCCCGAGTCTCATTTCTCGGTGCTGCTGAGATGAC 1176
 QY 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
 DB 1177 AGCTTTTGTGAGNAATTTTGGCGTGGTGGCAAAATCAGTAGATTCTTATTCAGAGAGCA 1236
 QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
 DB 1237 AAAGCCTCAATGGATGTGTTCTAGTGCACTGTGTAGCTGGGATCTCCCGCTCCGCCACC 1296

QY 106 IleAlaIleAlaTyPheMetLysArgMetAspMetSerLeuAspGluAlaTyArgPhe 125
 DB 1297 ATCGCTATCGCTACATCATGAAGAGGATGACATGTCTTTAGATGAAGCTTACAGATTT 1356
 QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
 DB 1357 GTGAAGAAGAAAGACCTTACTATATCTCCAACTTCAATTTCTGGGCCAATCTCTGGAC 1416
 QY 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
 DB 1417 TATGAGAAGAAGATTAAAGAACACAGCTGAGCATCGAGGCGCAAGAGCAAACTCAAGCTG 1476
 QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
 DB 1477 CTGCACCTGGAGAAAGCCAAATGAACCTGTCTGCTCTCAGAGGGTGGACAGAAAAGC 1536
 QY 186 GluThrProLeuSerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
 DB 1537 GAGAGCCCTTCAGTCCACCTGTGCCGACTCTGCTACCTCAGAGGAGAGGACAAAGG 1596
 QY 206 ProValHisProAlaSerValProSerValGlnProSerLeuLeuGluAsp 225
 DB 1597 CCGGTGCATCCCGCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCG 1656
 QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
 DB 1657 AGCCCGCTGGTACAGGGCTCAGTGGGCTGACCTGTCCGAGACAGCGTCCGAGACAGC 1716
 QY 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyPheSerAlaSerMet 265
 DB 1717 AATAAGCTCAAGCGTCTCTCTGATATCAATCAGTTTCATATTCAGCCAGCATG 1776
 QY 266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyPheTyPheProSer 285
 DB 1777 GCAGCATCTTACATGGCTTCTCTCATCAGAAGATGTTTGGATACTACAAACCTTCC 1836
 QY 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
 DB 1837 ACTACTCTGGATGGACCAACAAGCTATGCTCCAGTTCTCCCTGTTCCAGGAATCTACGAG 1896
 QY 306 GlnThrProGluThrSerProAspLysGluLysLeuAlaSerIleProLysLysLeuGlnThr 325
 DB 1897 CAGACTCCCGAAACAGTCTCTGATAAGAGAGAACCCAGCATCCCAAGAGAGCTCAGACC 1956
 QY 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
 DB 1957 GCCAGGCTTCAGACAGCAGCAGCAGGATGCGATTCGTCAGAACAGCAGCAGCAGCTGGC 2016
 QY 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyP 365
 DB 2017 ACCGCCAGAGTCCCTTTATCTCCATCGATCGAAGTGGAGCGTGGAGACAAATTC 2076
 QY 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
 DB 2077 CACACAGCTTCTCTTTCGGCTTTCCACAGCAGCAGCAGCAGCTTCAGGAAGTCTGCTGGC 2136
 QY 386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
 DB 2137 CTGGGCTTAAAGGCTGGCCTCGGATATCTTGGCCCCCAGAGCTCTTACCCCTTCCCTG 2196
 QY 406 ThrSerSerTrpTyPheAlaThrGluSerSerHisPheTyPheSerAlaSerAlaIleTyP 425
 DB 2197 ACCAGCAGCTGTGTTTGGCCAGAGTCTCCTCACTTCTACTTCTGCTCAGCCATCTAC 2256
 QY 426 GlyGlySerAlaSerTyPheAlaTyPheSerCysSerGlnLeuProThrCysGlyAspGln 445
 DB 2257 GGAGGAGTGGCAGTACTTCTGCTCAGCTGAGCAGCAGCTGCTGCCACTTCCGAGAGCAAA 2316
 QY 446 ValTyPheValArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
 DB 2317 GTCTATTCTGTGGCGAGCGGCAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2376
 QY 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485

883	AAAGCCTCCAATGGATGTGTTCTAGTCAGCTGCTTTAGCTGGGATCTCCGCGCTCCGCCACC	942
106	lleAlaIleAlaTyriIeMetIysArgMetAspMetSerLeuAspGluAlaTyriArgPhe	125
943	ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTCTTTAGATCAAGCTTTACAGATTT	1002
126	ValIysGluIysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp	145
1003	GTGAAGAGAAAAGAACCTTACTATATCTCCAACTTCAATTTTCTGGGCCAACTCTCTGGAC	1062
146	TyrGluIysIleIysAsnGlnThrGlyAlaSerGlyProIysSerIysLeuIysLeu	165
1063	TATGAGAAGAGATTAAAGACACAGCTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTG	1122
166	LeuHisLeuGluIysProAsnGluProValProAlaValSerGluGlyGlnIysSer	185
1123	CTGCACCTCGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGC	1182
186	GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg	205
1183	GAGACGCCCTCAGTGCACCCCTGTGCCGACTCTGTCTACCTCAGAGCGCAGCAGCAAAAG	1242
206	ProValHisProAlaSerValProSerValProSerValGlnProSerIleuLeuGluAsp	225
1243	CCCGTGCATCCCGCAGCGTCCACAGCTGCCAGCGTGCACCGCTGCAGCTGTTAGAGGAC	1302
226	SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer	245
1303	AGCCCGCTGGTACAGCGCTCAGTGGGCTGCACCTGTCCGCAGACAGGCTGGAGAAGACAG	1362
246	AsnIysLeuIysArgSerPheSerIleuAspIleIysSerValSerTyrSerAlaSerMet	265
1363	AATAAGCTCAAGCGTTCTCTCTCTGGAGATCAAAATCAGTTTTCATATTACGCCAGCATG	1422
266	AlaAlaSerIleuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrIysProSer	285
1423	GCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGATACTACAACCTTCC	1482
286	ThrThrLeuAspGlyThrAsnIysLeuCysGlnPheSerProValGlnGluLeuSerGlu	305
1483	ACTACTCTGGATGGGACCAACAGCTATSCCAGTTCTCCCTCTGTTCAGGAACATATCCGAG	1542
306	GlnThrProGluThrSerProAspIysGluGluAlaSerIleProIylsIysLeuGlnThr	325
1543	CAGACTCCCGAAACCACTGCTCTGATAGGAGGAAGCCAGCATCCCCAAAGAGCTGCAGACC	1602
326	AlaArgProSerAspSerGlnSerIysArgLeuHisSerValArgThrSerSerSerGly	345
1603	GCAGAGCCTTCACAGGCACAGACAAGCATTCGATTCGGTCAGAACCCAGCAGCATGGC	1662
346	ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr	365
1663	ACCGCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGGACAATTAC	1722
366	HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrIysSerAlaGly	385
1723	CACACCACTCTCCTTTTGGCCCTTTCACCGCCAGCAGCACCTCAGAACTGTGTCTGGC	1782
386	LeuGlyLeuIysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu	405
1783	CTGGGCCCTTAAGGGCTGGCACTCGAGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG	1842
406	ThrSerSerTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr	425
1843	ACACAGAGCTGGTATTTTGTGCCACAGAGTCTTCACATTTCTACTCTGCCTCAGCCATCTAC	1902
426	GlyGlySerAlaSerTyrSerAlaTyriSerCysSerGlnLeuProThrCysGlyAspGln	445
1903	GGAGGCAGTCCCAAGTTACTCTGTCTACAGCTGCAGCCAGCTGCGCCACTTCGCGAGACCAA	1962
446	ValTyrSerValArgArgGlnIysProSerAspArgAlaAspSerArgSerTyr	465
1963	GTCTATTCTGTGGCAGCGCGAGAGCCAAAGTCACAGACTGACTCGCGCGGAGCTGG	2022

Qy 466 HisGluGluSerProPheGluLysGlnPheLysArgSerCysGlnMetGluPheGly 485
 Db 2023 CATCAAGAGAGCCCTTTGAAAGCAGTTTAAACGCAGAGCTGCCAAATGGAAATTTGGA 2082
 Qy 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
 Db 2083 GAGAGCATCATGTGAGAGAAACAGGTCAACGGAGAGCTGGGGAAGTGGGCAGTCAGTCT 2142
 Qy 506 SerPheSerGlySerMetGluIleIleGluValSer 517
 Db 2143 AGCTTTTCGGGCAGCATGGAAATCATTTAGGTCTCC 2178

Search completed: September 24, 2004, 08:56:43
 Job time : 767 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

4 protein - protein search, using sw model

in on: September 23, 2004, 14:18:58 ; Search time 53 Seconds
(without alignments)
53.311 Million cell updates/sec

title: US-09-964-277-16
arfect score: 52
aquence: 1 VHCLAGISRS 10

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

sarched: 1586107 seqs, 282547505 residues

otal number of hits satisfying chosen parameters: 1586107

inimum DB seq length: 0
aximum DB seq length: 2000000000

3st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- atabase : A Genesep 29Jan04:*
- 1: genesep1980s:*
 - 2: genesep1990s:*
 - 3: genesep2000s:*
 - 4: genesep2001s:*
 - 5: genesep2002s:*
 - 6: genesep2003as:*
 - 7: genesep2003bs:*
 - 8: genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	23	5 ABR52406	AbR52406 Peptide r
2	52	100.0	23	5 ABR52380	AbR52380 Peptide r
3	52	100.0	41	5 AAU79157	AAU79157 Human EST
4	52	100.0	140	5 ABR52404	AbR52404 Peptide r
5	52	100.0	168	4 AAB66435	AAB66435 Human MAP
6	52	100.0	168	4 AAB66436	AAB66436 Human MAP
7	52	100.0	170	4 AAB66434	AAB66434 Human MAP
8	52	100.0	170	4 AAB66436	AAB66436 Human MAP
9	52	100.0	170	4 AAB66436	AAB66436 Human MAP
10	52	100.0	170	4 AAB66436	AAB66436 Human MAP
11	52	100.0	189	3 AAB53302	AbA53302 Human col
12	52	100.0	302	5 ABR52425	AbR52425 Protein r
13	52	100.0	317	7 ADC99098	ADC99098 Human KXP
14	52	100.0	322	4 AAG67635	AAG67635 Amino aci
15	52	100.0	322	4 AAG67456	AAG67456 Amino aci
16	52	100.0	368	5 AAE14240	AAE14240 Human pro
17	52	100.0	373	4 AAU31149	AAU31149 Novel hum
18	52	100.0	381	5 ABR52383	AbR52383 Protein r
19	52	100.0	381	6 ABP96803	ABP96803 Human COP
20	52	100.0	381	6 ABP57087	ABP57087 Mouse MXP
21	52	100.0	381	7 ADP48300	ADP48300 Rat Prote
22	52	100.0	381	7 ADP52625	ADP52625 Rat Prote
23	52	100.0	419	6 ABP55026	ABP55026 Human dua
24	52	100.0	517	5 AAU79159	AAU79159 Human dua
25	52	100.0	579	7 ADE08458	ADE08458 Novel pro

ALIGNMENTS

RESULT 1

ABR52406
ID ABR52406 standard; peptide; 23 AA.

XX ABR52406;

XX AC

XX 19-JUN-2003 (first entry)

XX DT

XX DE Peptide relating to the invention SEQ ID NO: 144.

XX KW antiproliferative; hepatotropic; nephrotropic; antiarthritic;
XX KW antipsoriatic; cardiant; cytostatic; gene therapy; liver disease;
XX KW proliferative disorder; renal failure; cardiovascular disorder;
XX KW immunological disorder; arthritis; psoriasis; congenital heart defect;
XX KW congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
XX OS Homo sapiens.

XX PN WO200257460-A2.

XX PD 25-JUL-2002.

XX PF 20-DEC-2001; 2001WO-US050459.

XX PR 20-DEC-2000; 2000US-0256868P.

XX PR 30-MAR-2001; 2001US-0280186P.

XX PR 01-MAY-2001; 2001US-0287735P.

XX PR 05-JUN-2001; 2001US-0295848P.

XX PR 25-JUN-2001; 2001US-0300465P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L;
XX PI Siemers N, Bol D, Schieven G, Finger J, Todderud CG, Bassolino D;
XX PI Krystek S, Mcatee P, Suchard S, Banas D;
XX WPI; 2002-599721/64.

XX PT Novel polynucleotides encoding human phosphatase polypeptides useful in
XX PT the prevention or treatment of e.g. proliferative and cardiovascular
XX PT disorders.

XX PS Disclosure; Page 174; 801pp; English.

XX CC The invention relates to a novel isolated nucleic acid comprising a
XX CC polynucleotide having a nucleotide sequence selected from 40

XX CC polynucleotides fully defined in the specification. The polynucleotide of
XX CC the invention has antiproliferative, hepatotropic, nephrotropic,

26 52 100.0 625 5 ABR52382
27 52 100.0 625 5 ABR52350
28 52 100.0 625 6 ABG73440
29 52 100.0 663 2 AAU29150
30 52 100.0 663 5 ABR52351
31 52 100.0 664 5 ABR52424
32 52 100.0 665 4 AAE04834
33 52 100.0 665 4 AAU09016
34 52 100.0 665 5 AAU79156
35 52 100.0 665 5 AAU79161
36 52 100.0 665 5 ABR52381
37 52 100.0 665 5 ABR52352
38 52 100.0 665 5 ABR52407
39 52 100.0 665 5 AAU09946
40 52 100.0 665 5 AAU75789
41 52 100.0 665 5 ABB97946
42 52 100.0 665 5 AAU79929
43 52 100.0 665 5 ABB97291
44 52 100.0 665 6 ADA54744
45 52 100.0 666 4 AAB20325

AbR52382 Protein r
AbR52350 Protein r
ABG73440 Human dua
AAU29150 Dual-spec
AbR52351 Protein r
AbR52424 Protein r
AAE04834 Human SGP
AAU09016 Human dua
AAU79156 Human dua
AAU79161 Human dua
ABR52381 Protein r
ABR52352 Protein r
ABR52407 Protein r
AAU09946 Protein s
AAU75789 Human pro
ABB97946 Human pro
AAU79929 Human qua
ABB97291 Novel hum
ADA54744 Human pro
AAB20325 Human pro

C cloning and sequencing cDNA encoding the human dual-specificity
C phosphatase-3 (DSP-16) protein of the invention

Q Sequence 41 AA;
Query Match 100.0%; Score 52; DB 5; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VHCLAGISRS 10
| | | | |
b 11 VHCLAGISRS 20

RESULT 4
BR52404
D ABR52404 standard; protein; 140 AA.
X
C ABR52404;
X
T 19-JUN-2003 (first entry)
X
E Peptide relating to the invention SEQ ID NO: 134.
X
W antiproliferative; hepatotropic; nephrotropic; antiarthritic;
M antipsoriatic; cardiant; cycostatic; gene therapy; liver disease;
N proliferative disorder; renal failure; cardiovascular disorder;
M immunological disorder; arthritis; psoriasis; congenital heart defect;
X congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.

S Homo sapiens.
K WO200257460-A2.
N
D 25-JUL-2002.
C
? 20-DEC-2001; 2001WO-US050459.
C
C 20-DEC-2000; 2000US-0256868P.
C 30-MAR-2001; 2001US-0280186P.
C 01-MAY-2001; 2001US-0287735P.
C 05-JUN-2001; 2001US-0295848P.
C 25-JUN-2001; 2001US-0300465P.
C (BRIM) BRISTOL-MYERS SQUIBB CO.
C Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L;
C Siemers N, Bol D, Schieven G, Finger J, Todderud CG, Bassolino D;
C Kryatek S, Mcatee P, Suchard S, Banas D;
C WPI; 2002-599721/64.

Novel polynucleotides encoding human phosphatase polypeptides useful in the prevention or treatment of e.g. proliferative and cardiovascular disorders.

Disclosure, Page 164; 801pp; English.
The invention relates to a novel isolated nucleic acid comprising a polynucleotide having a nucleotide sequence selected from 40 polynucleotides fully defined in the specification. The polynucleotide of the invention has antiproliferative, hepatotropic, nephrotropic, antiarthritic, antipsoriatic, cardiant, and cycostatic activity. The polynucleotide may have a use in gene therapy. A polynucleotide or polypeptide of the invention is useful for preventing, treating or ameliorating a medical condition, e.g. a proliferative disorder. They are also useful for treating e.g. liver disease, renal failure, immunological disorders including arthritis and psoriasis, cardiovascular disorders such as congenital heart defects and congestive heart failure, and cancer. A method of the invention is useful for diagnosing a pathological condition or susceptibility to a condition in a subject. The present sequence is used in the exemplification of the invention

SQ Sequence 140 AA;

Query Match 100.0%; Score 52; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.035; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | |
Db 85 VHCLAGISRS 94

RESULT 5
AAB66435
ID AAB66435 standard; protein; 168 AA.
XX
AC AAB66435;
XX
DT 06-APR-2001 (first entry)
XX
DE Human MAP-kinase phosphatase MKP-7.
XX
KW Human; MAP-kinase; mitogen-activated protein kinase; DSP-3; cycostatic;
KW immunosuppressive; antiallergic; dual specificity phosphatase-3;
KW cell proliferation; metabolic diseases; Duchenne muscular dystrophy;
KW cancer; graft-versus-host disease; autoimmune disease; allergy; MKP-7.
XX
OS Homo sapiens.

PN WO200102582-A1.
XX
PD 11-JAN-2001.

XX 29-JUN-2000; 2000WO-US018207.

XX 02-JUL-1999; 99US-0142338P.

PR 07-APR-2000; 2000WO-US009185.

PR 20-APR-2000; 2000WO-US010868.

XX (CEPT-) CEPTVR INC.

XX Luche RM, Wei B;

XX WPI; 2001-138149/14.

XX New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form polypeptides, useful for identifying modulators DSP-3 or DSP-3 alternate form activity, especially for treating e.g. cancer, autoimmune diseases or allergies.

XX Example 1; Fig 3; 86pp; English.

CC The present sequence is given in a specification providing human dual specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide. The polypeptides are useful for dephosphorylating a substrate of DSP-3, e.g. MAP-kinase. They may be used to treat or prevent diseases associated with cell proliferation, immunosuppression, metabolic diseases, or abnormal cell growth or cell cycle abnormalities. They are also useful for identifying agents that modulate their activity. The modulators are useful for treating disorders associated with DSP-3 or DSP-3 variant activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities. The modulating agents are useful for modulating, modifying or altering cellular responses, e.g. in vivo or in vitro cell proliferation, differentiation or survival. The present sequence was used in homology studies with DSP-3 and other MAP-kinase phosphatases

XX Sequence 168 AA;

Query Match 100.0%; Score 52; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.042; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VHCLAGISRS 10	
DB	108	VHCLAGISRS 117	
RESULT 6			
AAE06778			
ID	AAE06778	standard; protein; 168 AA.	
XX	AC	AAE06778;	
XX	DT	16-OCT-2001 (first entry)	
XX	DE	Human dual-specificity phosphatase (DSP) protein, MKP-7.	
XX	KW	Human; dual-specificity phosphatase; DSP; dual phosphorylation motif;	
XX	KW	mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease;	
XX	KW	GVHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease;	
XX	KW	allergy; metabolic disease; cell growth; cell proliferation; cytostatic;	
XX	KW	cell cycle abnormality; cell differentiation; antiallergic; muscular;	
XX	OS	immunosuppressive.	
XX	OS	Homo sapiens.	
XX	PN	WO200157221-A2.	
XX	PD	09-AUG-2001.	
XX	PF	01-FEB-2001; 2001WO-US003429.	
XX	PR	02-FEB-2000; 2000US-0179886P.	
XX	PA	(CEPT-) CEPTYR INC.	
XX	PI	Lucie RM, Wei B;	
XX	WPI	2001-48887/53.	
XX	DR	New isolated dual-specificity phosphatase polypeptide for treating	
XX	PT	cancer, graft-versus-host disease, autoimmune diseases, allergies,	
XX	PT	metabolic diseases, abnormal cell growth and abnormal cell proliferation.	
XX	PS	Example 1; Fig 6; 81pp; English.	
XX	CC	The present sequence is human dual-specificity phosphatase (DSP) protein,	
XX	CC	MKP-7. MKP-7 is used to derive a longer consensus DSP amino acid	
XX	CC	sequences motif that would be useful for the identification of new DSP	
XX	CC	family members. Inactivation of mitogen-activated protein kinase (MAP-	
XX	CC	kinase) is mediated by dephosphorylation at a dual phosphorylation motif	
XX	CC	by DSP which is referred to as MAP-kinase phosphatase. An agent that	
XX	CC	modulates DSP is useful for treating a disorder selected from Duchenne	
XX	CC	muscular dystrophy, cancer, graft-versus-host disease (GVHD), autoimmune	
XX	CC	diseases, allergies, metabolic diseases, abnormal cell growth, abnormal	
XX	CC	cell proliferation and cell cycle abnormalities. DSP is useful for	
XX	CC	identifying antibodies and other agents that inhibit DSP-12 and/or DSP-13	
XX	CC	activity. DSP and the agents identified are useful for modulating cell	
XX	CC	proliferation, differentiation and survival. DSP is useful in screening	
XX	CC	assays for modulators of enzyme activity and substrate binding and for	
XX	CC	dephosphorylating a substrate of DSP-12 or DSP-13	
XX	SQ	Sequence 168 AA;	
	Query Match	100.0%; Score 52; DB 4; Length 168;	
	Best Local Similarity	100.0%; Pred. No. 0.042;	
	Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	VHCLAGISRS 10	
DB	108	VHCLAGISRS 117	
RESULT 7			
AAB66434			
ID	AAB66436	standard; protein; 170 AA.	
XX	AC	AAB66436;	
XX	DT	06-APR-2001 (first entry)	
XX	OS	Homo sapiens.	
XX	PN	WO200102582-A1.	
XX	PD	11-JAN-2001.	
XX	PF	29-JUN-2000; 2000WO-US018207.	
XX	PR	02-JUL-1999; 99US-0142338P.	
XX	PR	07-APR-2000; 2000WO-US009185.	
XX	PR	20-APR-2000; 2000WO-US010868.	
XX	PA	(CEPT-) CEPTYR INC.	
XX	PI	Lucie RM, Wei B;	
XX	WPI	2001-138149/14.	
XX	DR	New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form	
XX	PT	polypeptides, useful for identifying modulators DSP-3 or DSP-3 alternate	
XX	PT	form activity, especially for treating e.g. cancer, autoimmune diseases	
XX	PT	or allergies.	
XX	PS	Example 1; Fig 3; 86pp; English.	
XX	CC	The present sequence is given in a specification providing human dual	
XX	CC	specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide.	
XX	CC	The polypeptides are useful for dephosphorylating a substrate of DSP-3,	
XX	CC	e.g. MAP-kinase. They may be used to treat or prevent diseases associated	
XX	CC	with cell proliferation, immunosuppression, metabolic diseases, or	
XX	CC	abnormal cell growth or cell cycle abnormalities. They are also useful	
XX	CC	for identifying agents that modulate their activity. The modulators are	
XX	CC	useful for treating disorders associated with DSP-3 or DSP-3 variant	
XX	CC	activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host	
XX	CC	disease, autoimmune diseases, allergies, metabolic diseases, abnormal	
XX	CC	cell growth, abnormal cell proliferation and cell cycle abnormalities.	
XX	CC	The modulating agents are useful for modulating, modifying or altering	
XX	CC	cellular responses, e.g. in vivo or in vitro cell proliferation,	
XX	CC	differentiation or survival. The present sequence was used in homology	
XX	CC	studies with DSP-3 and other MAP-kinase phosphatases	
XX	SQ	Sequence 170 AA;	
	Query Match	100.0%; Score 52; DB 4; Length 170;	
	Best Local Similarity	100.0%; Pred. No. 0.043;	
	Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	VHCLAGISRS 10	
DB	110	VHCLAGISRS 119	
RESULT 8			
AAB66436			
ID	AAB66436	standard; protein; 170 AA.	
XX	AC	AAB66436;	
XX	DT	06-APR-2001 (first entry)	

B Human MAP-kinase phosphatase hVH5.
K Human; MAP-kinase; mitogen-activated protein kinase; DSP-3; cytostatic;
N immunosuppressive; antiallergic; dual specificity phosphatase-3;
N cell proliferation; metabolic diseases; Duchenne muscular dystrophy;
N cancer; graft-versus-host disease; autoimmune disease; allergy; hVH5.
S Homo sapiens.
K WO200102582-A1.
N 11-JAN-2001.
D 29-JUN-2000; 2000WO-US018207.
F 02-JUL-1999; 99US-0142338P.
R 07-APR-2000; 2000WO-US009185.
R 20-APR-2000; 2000WO-US010868.
K (CEPT-) CEPTYR INC.
K Luche RM, Wei B;
I WPI; 2001-138149/14.
R New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form
I polypeptides, useful for identifying modulators DSP-3 or DSP-3 alternate
I form activity, especially for treating e.g. cancer, autoimmune diseases
I or allergies.
K Example 1; Fig 3; 86pp; English.
K The present sequence is given in a specification providing human dual
K specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide.
K The polypeptides are useful for dephosphorylating a substrate of DSP-3,
K e.g. MAP-kinase. They may be used to treat or prevent diseases associated
K with cell proliferation, immunosuppression, metabolic diseases, or
K abnormal cell growth or cell cycle abnormalities. They are also useful
K for identifying agents that modulate their activity. The modulators are
K useful for treating disorders associated with DSP-3 or DSP-3 variant
K activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host
K disease, autoimmune diseases, allergies, metabolic diseases, abnormal
K cell growth, abnormal cell proliferation and cell cycle abnormalities.
K The modulating agents are useful for modulating, modifying or altering
K cellular responses, e.g. in vivo or in vitro cell proliferation,
K differentiation or survival. The present sequence was used in homology
K studies with DSP-3 and other MAP-kinase phosphatases
K Sequence 170 AA;
D Query Match 100.0%; Score 52; DB 4; Length 170;
D Best Local Similarity 100.0%; Pred. No. 0.043;
D Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 VHCLAGISRS 10
D |||||
D 110 VHCLAGISRS 119
D
D RESULT 9
D AE06780
D AAE06780 standard; protein; 170 AA.
K AAE06780;
K 16-OCT-2001 (first entry)
E Human dual-specificity phosphatase (DSP) protein, hVH5.
K Human; dual-specificity phosphatase; DSP; dual phosphorylation motif;
K mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease;
K GVHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease;
K allergy; metabolic disease; cell growth; cell proliferation; cytostatic;
N

KW cell cycle abnormality; cell differentiation; antiallergic; muscular;
KW immunosuppressive.
XX Homo sapiens.
XX WO200157221-A2.
XX 09-AUG-2001.
XX 01-FEB-2001; 2001WO-US003429.
XX 02-FEB-2000; 2000US-0179886P.
XX (CEPT-) CEPTYR INC.
XX Luche RM, Wei B;
XX WPI; 2001-488887/53.
XX New isolated dual-specificity phosphatase polypeptide for treating
PT cancer, graft-versus-host disease, autoimmune diseases, allergies,
PT metabolic diseases, abnormal cell growth and abnormal cell proliferation.
XX Example 1; Fig 6; 81pp; English.
XX The present sequence is human dual-specificity phosphatase (DSP) protein,
CC hVH5. hVH5 is used to derive a longer consensus DSP amino acid sequences
CC motif that would be useful for the identification of new DSP family
CC members. Inactivation of mitogen-activated protein kinase (MAP-kinase)
CC is mediated by dephosphorylation at a dual phosphorylation motif by DSP
CC which is referred to as MAP-kinase phosphatase. An agent that modulates
CC DSP is useful for treating a disorder selected from Duchenne muscular
CC dystrophy, cancer, graft-versus-host disease (GVHD), autoimmune diseases,
CC allergies, metabolic diseases, abnormal cell growth, abnormal cell
CC proliferation and cell cycle abnormalities. DSP is useful for identifying
CC antibodies and other agents that inhibit DSP-12 and/or DSP-13 activity.
CC DSP and the agents identified are useful for modulating cell
CC proliferation, differentiation and survival. DSP is useful in screening
CC assays for modulators of enzyme activity and substrate binding and for
CC dephosphorylating a substrate of DSP-12 or DSP-13
XX Sequence 170 AA;
SQ Query Match 100.0%; Score 52; DB 4; Length 170;
SQ Best Local Similarity 100.0%; Pred. No. 0.043;
SQ Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VHCLAGISRS 10
D |||||
D 110 VHCLAGISRS 119
D
D RESULT 10
D AAE06777
D ID AAE06777 standard; protein; 170 AA.
XX AAE06777;
XX 16-OCT-2001 (first entry)
XX Human dual-specificity phosphatase (DSP) protein, PYST1.
XX Human; dual-specificity phosphatase; DSP; dual phosphorylation motif;
KW mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease;
KW GVHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease;
KW allergy; metabolic disease; cell growth; cell proliferation; cytostatic;
KW cell cycle abnormality; cell differentiation; antiallergic; muscular;
KW immunosuppressive.
XX Homo sapiens.
XX WO200157221-A2.
XX

PD	09-AUG-2001.
XX	
PF	01-FEB-2001; 2001WO-US003429.
XX	
PR	02-FEB-2000; 2000US-0179886P.
XX	
PA	(CEPT-) CBFTYR INC.
PI	Luche RM, Wei B;
PI	
DR	WPI; 2001-488887/53.
XX	
PT	New isolated dual-specificity phosphatase polypeptide for treating
PT	cancer, graft-versus-host disease, autoimmune diseases, allergies,
PT	metabolic diseases, abnormal cell growth and abnormal cell proliferation.
XX	
PS	Example 1; Fig 6; 8ipp; English.
XX	
CC	The present sequence is human dual-specificity phosphatase (DSP) protein,
CC	pysr1. pysr1 is used to derive a longer consensus DSP amino acid
CC	sequences motif that would be useful for the identification of new DSP
CC	family members. Inactivation of mitogen-activated protein kinase (MAP-
CC	kinase) is mediated by dephosphorylation at a dual phosphorylation motif
CC	by DSP which is referred to as MAP-kinase phosphatase. An agent that
CC	modulates DSP is useful for treating a disorder selected from Duchenne
CC	DSP muscular dystrophy, cancer, graft-versus-host disease (GVHD), autoimmune
CC	diseases, allergies, metabolic diseases, abnormal cell growth, abnormal
CC	cell proliferation and cell cycle abnormalities. DSP is useful for
CC	identifying antibodies and other agents that inhibit DSP-12 and/or DSP-13
CC	activity. DSP and the agents identified are useful for modulating cell
CC	proliferation, differentiation and survival. DSP is useful in screening
CC	assays for modulators of enzyme activity and substrate binding and for
CC	dephosphorylating a substrate of DSP-12 or DSP-13
XX	
XX	Sequence 170 AA:
SQ	

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM;
WPI: 2000-587534/55.
DR N-PSDB; AAC98059.
Colo cancer associated gene sequences, referred to as colo cancer
antigens, useful for the treatment, prevention, and diagnosis of colo
disorders such as colo cancer.
Claim 11; Page 1391-1392; 2104pp; English.
AAC97991 to AAC98763 encode the human colo cancer associated proteins,
called human colo cancer antigens, given in AAB53234 to AAB54006. The
human colo cancer antigens can have cytostatic, gastroactive, muscular,
neuroprotective, immunomodulatory, gynecological, gastrointestinal,
vulnary, nephrotropic, antinefctive and antibacterial activities, and
can be used in gene therapy. The colo cancer antigen polynucleotides,
proteins and antibodies to the proteins are useful for the prevention,
treatment and diagnosis of colo disorders, such as colo cancer. The
polynucleotides may be used in diagnostics and research, such as for
chromosome identification, and as hybridisation probes. The proteins may
also be used to prevent diseases such as neural disorders, immune system
disorders, muscular disorders, reproductive disorders, gastrointestinal
disorders, wounds, renal disorders, infectious diseases, and
cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
sequences used in the exemplification of the present invention
Sequence 189 AA;
Query Match 100.0%; Score 52; DB 3; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match          100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. NO. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VHCLAGISRS 10
    |||||
Db 110 VHCLAGISRS 119

RESULT 11
AAB53302
ID AAB53302 standard; protein; 189 AA.
XX AAB53302;
XX AC
XX AC
DT 09-MAR-2001 (first entry)
XX
XX Human colon cancer antigen protein sequence SEQ ID NO:842.
DE
XX Human: colon cancer; colon cancer antigen; diagnosis; detection;
XX identification; cytostatic; cardioactive; neuroprotective; vulnery;
XX immunomodulatory; muscular; gynaecological; gastrointestinal;
XX nephrotropic; antinefctive; antibacterial; gene therapy; wound;
XX neural disorder; immune system disorder; muscular disorder;
XX reproductive disorder; gastrointestinal disorder; renal disorder;
XX infectious disease; cardiovascular disorder.
XX
XX Homo sapiens.
OS
XX WO200055351-A1.
XX
XX
XX
XX
XX 21-SEP-2000.
XX
XX
XX 08-MAR-2000; 2000MO-US005883.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX

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Siemers N, Bol D, Schieven G, Finger J, Todderud CG, Bassolino D;
Kryetsek S, Mcatee P, Suchard S, Banas D;
WPI; 2002-599721/64.
Novel polynucleotides encoding human phosphatase polypeptides useful in
the prevention or treatment of e.g. proliferative and cardiovascular
disorders.
Example 57; Page 501; 801pp; English.
The invention relates to a novel isolated nucleic acid comprising a
polynucleotide having a nucleotide sequence selected from 40
polynucleotides fully defined in the specification. The polynucleotide of
the invention has antiproliferative, hepatotropic, nephrotropic,
antiarthritic, antipsoriatic, cardiac, and cytostatic activity. The
polynucleotide may have a use in gene therapy. A polynucleotide or
polypeptide of the invention is useful for preventing, treating or
ameliorating a medical condition, e.g. a proliferative disorder. They are
also useful for treating e.g. liver disease, renal failure, immunological
disorders including arthritis and psoriasis, cardiovascular disorders
such as congenital heart defects and congestive heart failure, and
cancer. A method of the invention is useful for diagnosing a pathological
condition or susceptibility to a condition in a subject. The present
sequence is used in the exemplification of the invention
Sequence 302 AA;
Query Match 100.0%; Score 52; DB 5; Length 302;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VHCLAGISRS 10
|||||
242 VHCLAGISRS 251
RESULT 13
JC99098
ADC99098 standard; protein; 317 AA.
ADC99098;
01-JAN-2004 (first entry)
Human KPP protein - SEQ ID 51.
anti-HIV; anti-allergic; anti-inflammatory; antianaemic; antiparkinsonian;
nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
cancer; developmental; mental retardation; neurological;
Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
helminthic infection; transgenic; gene therapy; human; enzyme.
Homo sapiens.
WO2003033680-A2.
24-APR-2003.
17-OCT-2002; 2002WO-US033723.
19-OCT-2001; 2001US-0345474P.
02-NOV-2001; 2001US-0343910P.
13-NOV-2001; 2001US-0333098P.
16-NOV-2001; 2001US-0332424P.
30-NOV-2001; 2001US-0334288P.

(INCY-) INCYTE GENOMICS INC.
Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
Lindquist BA, Lu DM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
Rankumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
Thornton MB, Tran UK, Chawia NK, Warren BA, Yang J, Yao MG, Yue H;
Zebardjian Y;
WPI; 2003-403214/38.
N-PSDB; ADC99150.
New human kinases and phosphatases and polynucleotides, useful for
diagnosing, treating or preventing autoimmune or inflammatory disorders
(e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
cancer or hepatitis.
Claim 1; SEQ ID NO 51; 424pp; English.
The invention relates to a novel isolated polypeptide which is a human
kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
agonists and antagonists are useful for diagnosing, treating or
preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
retardation, neurological disorders including Alzheimer's disease and
Parkinson's disease, autoimmune and inflammatory disorders such as
Crohn's disease and diabetes mellitus and finally, viral, bacterial,
fungal, parasitic, protozoan or helminthic infections. Furthermore, the
polynucleotides encoding KPP may be useful for creating transgenic
animals to model human disease, as well as during gene therapy
procedures. The current sequence is that of the human KPP protein of the
invention.
Sequence 317 AA;
Query Match 100.0%; Score 52; DB 7; Length 317;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VHCLAGISRS 10
|||||
227 VHCLAGISRS 236
RESULT 14
AAG67635
ID AAG67635 standard; protein; 322 AA.
AC AAG67635;
DT 26-NOV-2001 (first entry)
DE Amino acid sequence of a human protein.
KW Human; protein kinase; protein phosphatase; signal transduction.
OS Homo sapiens.
PN WO200109316-A1.
PD 08-FEB-2001.
PF 28-JUL-2000; 2000WO-JP005061.
XX 29-JUL-1999; 99JP-00248036.
PR 18-OCT-1999; 99US-0159590P.
PR 11-JAN-2000; 2000JP-00118776.
PR 17-FEB-2000; 2000US-0183322P.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX

PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu J;
 XX
 DR WPI; 2001-570286/64.
 XX
 PT New genes encoding proteins with protein kinase/protein phosphatase
 PT activity, useful in the diagnosis and treatment of diseases.
 XX
 PS Example 4; Page 199-201; 233pp; Japanese.
 XX
 CC The specification describes human protein kinase/protein phosphatases. It
 CC is expected that the protein kinase/protein phosphatase gene participates
 CC in signal transduction in cells. The protein kinase/protein phosphatase
 CC polypeptides and polynucleotides are useful for developing diagnostics
 CC and treatment agents for human and animal diseases. The protein
 CC kinase/protein phosphatase polypeptides are useful as target molecules in
 CC designing novel drugs. The protein kinase/protein phosphatase
 CC polynucleotides are useful as a source of probes and primers, which may
 CC be used to isolate homologous sequences. The present sequence represents
 CC a human protein, which is used in the course of the invention
 XX
 SQ Sequence 322 AA;

Query Match 100.0%; Score 52; DB 4; Length 322;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 DB 232 VHCLAGISRS 241
 |||||

RESULT 15
 AAG67456
 ID AAG67456 standard; protein; 322 AA.
 XX
 AC AAG67456;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of a human polypeptide.
 XX
 KW Human; protein kinase; protein phosphatase; signal transduction;
 KW intracellular signalling pathway.
 XX
 OS Homo sapiens.
 XX
 PN WO200109345-A1.
 XX
 PD 08-FEB-2001.
 XX
 PF 28-JUL-2000; 2000WO-JP005060.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 18-OCT-1999; 99US-0159590P.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 17-FEB-2000; 2000US-0183322P.
 PR 02-MAY-2000; 2000JP-00183767.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu J;
 XX
 DR WPI; 2001-564736/63.
 XX
 PT New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes.

XX Example 4; Page 299-301; 336pp; Japanese.
 PS
 XX The specification describes human protein kinase/protein phosphatases.
 CC The polypeptides are expected to participate in signal transduction in
 CC cells. The kinase phosphatases are connected with intracellular
 CC signalling pathways. Antisense oligonucleotides and compounds identified
 CC by screening (agonists or antagonists) can be used to treat human or
 CC animal disorders associated with the expression or function of the
 CC protein. In addition, the polypeptides may be used as target molecules
 CC for drug development. The present sequence represents a polypeptide, used
 CC in the course of the invention
 XX
 SQ Sequence 322 AA;
 Query Match 100.0%; Score 52; DB 4; Length 322;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHCLAGISRS 10
 DB 232 VHCLAGISRS 241
 |||||

Search completed: September 23, 2004, 14:20:19
 Job time : 56 secs

GenCore version 5.1.6
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4 protein - protein search, using sw model

on: September 23, 2004, 14:18:59 : Search time 16 Seconds

(without alignments)
60.120 Million cell updates/sec

title: US-09-964-277-16

arfect score: 52

Sequence: 1 VHCLAGISRS 10

oring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

sarched: 283366 seqs, 96191526 residues

otal number of hits satisfying chosen parameters: 283366

imum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

PIR 78:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	% Match	Length	DB ID	Description
1	52	100.0	276	T48906	protein-tyrosine-p
2	52	100.0	365	T32494	hypothetical prote
3	51	98.1	619	T15969	hypothetical prote
4	49	94.2	272	T18915	hypothetical prote
5	48	92.3	226	T21380	hypothetical prote
6	48	92.3	330	T39698	protein tyrosine p
7	46	88.5	142	T03074	dual specificity p
8	46	88.5	169	T30684	probable dual spec
9	46	88.5	169	AF3412	hypothetical prote
10	46	88.5	303	T46405	hypothetical prote
11	46	88.5	314	A57126	dual specificity p
12	46	88.5	314	B57126	dual specificity p
13	46	88.5	367	S29090	dual specificity p
14	46	88.5	367	S24411	dual specificity p
15	46	88.5	367	S52265	dual specificity p
16	46	88.5	393	A56947	dual specificity p
17	46	88.5	394	A56115	dual specificity p
18	45	86.5	171	I36845	dual specificity p
19	45	86.5	171	T28522	probable dual spec
20	45	86.5	171	B72161	JiL protein - vari
21	45	86.5	272	T19418	hypothetical prote
22	45	86.5	384	I38900	dual specificity p
23	45	86.5	580	T18439	hypothetical prote
24	45	86.5	600	T18446	probable protein-c
25	45	86.5	807	S44538	hypothetical prote
26	44	84.6	165	A11187	hypothetical prote
27	44	84.6	165	A11545	hypothetical prote
28	44	84.6	1165	T15279	hypothetical prote
29	43	82.7	171	QQVZHI	dual specificity p

30 43 82.7 171 1 A42514 dual specificity p
31 43 82.7 171 1 B47452 dual specificity p
32 42 80.8 160 2 T10278 protein tyrosine p
33 42 80.8 167 2 JC5981 prenylated protein
34 42 80.8 356 2 JW0049 protein-tyrosine-p
35 42 80.8 377 1 A48711 protein-tyrosine-p
36 42 80.8 432 1 JN0317 protein-tyrosine-p
37 42 80.8 432 1 A34845 protein-tyrosine-p
38 42 80.8 435 1 TPUN1 protein-tyrosine-p
39 42 80.8 535 2 A46101 protein-tyrosine-p
40 42 80.8 548 2 B46101 protein-tyrosine-p
41 42 80.8 866 2 P88481 protein Cl6A3.1 [i
42 42 80.8 934 2 H88391 protein R06B10.2 [i
43 41 78.8 130 2 T29155 hypothetical prote
44 41 78.8 220 2 JC7885 low-molecular-mass
45 41 78.8 363 1 S14294 protein-tyrosine-p

ALIGNMENTS

RESULT 1

T48906

protein-tyrosine-phosphatase (EC 3.1.3.48) [imported] - Chlamydomonas eugametos
C:Species: Chlamydomonas eugametos

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000

C:Accession: T48906

R:Haring, M.A.; Siderius, M.; Joank, C.; Hirt, H.; Walton, K.M.; Musgrave, A.

Plant J. 7, 981-988, 1995

A:Title: Tyrosine phosphatase signalling in a lower plant: cell-cycle and oxidative str

A:Reference number: Z25005; MUID:95323001; PMID:7599654

A:Accession: T48906

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-276 <HAR>

A:Cross-references: EMBL:X77938; NID:G992593; PIDN:CAA54910.1; PID:G992594

A:Experimental source: strain UTREX 10

C:Genetics:

A:Gene: VH-PTP13

C:Keywords: phosphoric monoester hydrolase

Query Match 100.0%; Score 52; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10

DB 170 VHCLAGISRS 179

RESULT 2

T32494

hypothetical protein C05B10.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T32494

R:Geisel, C.; Wamsley, P.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C05B10.

A:Reference number: Z21178

A:Accession: T32494

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-365 <GEI>

A:Cross-references: EMBL:AF036685; PIDN:AA88308.1; GSPDB:GN00022; CESP:C05B10.1

A:Experimental source: strain Bristol N2; clone C05B10

C:Genetics:

A:Gene: CESP:C05B10.1

A:Map position: 4

A:Introns: 22/2; 46/2; 74/3; 163/2; 204/2; 248/1; 287/2

Query Match 100.0%; Score 52; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 |||||
 Db 265 VHCLAGISRS 274

RESULT 3

T15969

hypothetical protein F08B1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15969

R:Chissee, S.

submitted to the EMBL Data Library, July 1995

A:Description: The sequence of C. elegans cosmid F08B1.

A:Reference number: Z18439

A:Accession: T15969

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-619 <CHI>

A:Cross-references: EMBL:U23178; NID:g726421; PID:g726422; PIDN:AAC46719.1; CESP:F08B1.1

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F08B1.1

A:Introns: 22/2; 57/1; 99/1; 160/3; 252/2; 549/3

Query Match 98.1%; Score 51; DB 2; Length 619;

Best Local Similarity 90.0%; Pred. No. 0.055;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10

|||||

Db 222 VHCLAGISRS 231

RESULT 4

T18915

hypothetical protein C04F12.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T18915

R:Lloyd, C.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19044

A:Accession: T18915

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-272 <WIL>

A:Cross-references: EMBL:Z81451; PIDN:CAB03837.1; GSPDB:GN00019; CESP:C04F12.8

A:Experimental source: clone C04F12

C:Genetics:

A:Gene: CESP:C04F12.8

A:Map position: 1

A:Introns: 53/1; 84/3; 204/2

Query Match 94.2%; Score 49; DB 2; Length 272;

Best Local Similarity 80.0%; Pred. No. 0.063;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10

|||||

Db 92 VHCLAGISRS 101

RESULT 5

T21380

hypothetical protein F26A3.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21380

R:McMurray, A.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19415

A:Accession: T21380

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-226 <WIL>

A:Cross-references: EMBL:Z78419; PIDN:CAB01700.1; GSPDB:GN00019; CESP:F26A3.4

A:Experimental source: clone F26A3

C:Genetics:

A:Gene: CESP:F26A3.4

A:Map position: 1

A:Introns: 117/2; 150/3; 186/3

Query Match 92.3%; Score 48; DB 2; Length 226;

Best Local Similarity 80.0%; Pred. No. 0.083;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10

|||||

Db 96 VHCLAGISRS 105

RESULT 6

T39698

protein tyrosine phosphatase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T39698

R:Wood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, July 1999

A:Reference number: Z21870

A:Accession: T39698

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-330 <WOO>

A:Cross-references: EMBL:AL109652; PIDN:CAB51765.1; GSPDB:GN00067

A:Experimental source: strain 972h; cosmid c17A3

C:Genetics:

A:Gene: pi041

A:Map position: 2

Query Match 92.3%; Score 48; DB 2; Length 330;

Best Local Similarity 90.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10

|||||

Db 129 VHCLAGISRS 138

RESULT 7

T03074

dual specificity phosphoprotein phosphatase homolog - Chilo iridescent virus

C:Species: Chilo iridescent virus

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999

C:Accession: T03074

R:Bahr, U.; Tidona, C.A.; Darai, G.

Virus Genes 15, 235-245, 1997

A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates

A:Reference number: Z14834; MUID:98141693; PMID:9482599

A:Accession: T03074

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-142 <BAH>

A:Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94448.1; PID:g2738421

Query Match 88.5%; Score 46; DB 2; Length 142;

Best Local Similarity 90.0%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10

|||||

Db 79 VHCLAGISRS 88

STATUS: Preliminary
A:Molecule type: mRNA
A:Residues: 1-303 <AAA>
A:Cross-references: EMBL:AL137704
A:Experimental source: adult testis; clone DKFZp434O1321
C:Genetics:
A:Note: DKFZp434O1321.1

Query Match 88.5%; Score 46; DB 2; Length 303;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCAGISRS 10
||| |||||
Db 187 VHCAGISRS 196

RESULT 11
A57126
Dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 2 - human
N:Alternate names: mitogen-induced nuclear tyrosine phosphatase; phosphatase of activated T-cells
C:Species: Homo sapiens (man)
C:Date: 03-Nov-1995 #sequence_revision 02-Jul-1996 #text_change 11-Jun-1999
C:Accession: A57126
R:Rohan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Kruttsch, H.; Siebenlist, U.; Kel, Science 259, 1763-1766, 1993
A:Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
A:Reference number: A57126; MUID:93206122; PMID:7681221
A:Accession: A57126
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-314 <ROH>
A:Cross-references: GB:L11329; NID:G559539; PIDN:AAA50779.1; PID:G292376
C:Genetics:
A:Gene: GDB:DUSP2
A:Cross-references: GDB:I39200
A:Map position: 2q11-2q11
C:Function:
A:Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine, a C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity C:Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase
F:140-160/Region: nuclear location signal
F:180-311/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
F:257/Active site: Cys (phosphocysteine intermediate) #status predicted
F:263/Binding site: substrate phosphate (Arg) #status predicted

Query Match 88.5%; Score 46; DB 1; Length 314;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCAGISRS 10
||| |||||
Db 255 VHCAGISRS 264

RESULT 12
B57126
Dual specificity phosphatase (EC 3.1.3.-) 2 - mouse
N:Alternate names: mitogen-induced nuclear protein-tyrosine-phosphatase PAC-1
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 24-Apr-1998
C:Accession: B57126
R:Rohan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Kruttsch, H.; Siebenlist, U.; Kel, Science 259, 1763-1766, 1993
A:Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
A:Reference number: A57126; MUID:93206122; PMID:7681221
A:Accession: B57126
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-314 <ROH>
A:Cross-references: GB:L11330
C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity C:Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase

STATUS: Preliminary
A:Molecule type: mRNA
A:Residues: 1-303 <AAA>
A:Cross-references: EMBL:AL137704
A:Experimental source: adult testis; clone DKFZp434O1321
C:Genetics:
A:Note: DKFZp434O1321.1

Query Match 88.5%; Score 46; DB 2; Length 303;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCAGISRS 10
||| |||||
Db 187 VHCAGISRS 196

RESULT 11
A57126
Dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 2 - human
N:Alternate names: mitogen-induced nuclear tyrosine phosphatase; phosphatase of activated T-cells
C:Species: Homo sapiens (man)
C:Date: 03-Nov-1995 #sequence_revision 02-Jul-1996 #text_change 11-Jun-1999
C:Accession: A57126
R:Rohan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Kruttsch, H.; Siebenlist, U.; Kel, Science 259, 1763-1766, 1993
A:Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
A:Reference number: A57126; MUID:93206122; PMID:7681221
A:Accession: A57126
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-314 <ROH>
A:Cross-references: GB:L11329; NID:G559539; PIDN:AAA50779.1; PID:G292376
C:Genetics:
A:Gene: GDB:DUSP2
A:Cross-references: GDB:I39200
A:Map position: 2q11-2q11
C:Function:
A:Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine, a C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity C:Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase
F:140-160/Region: nuclear location signal
F:180-311/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
F:257/Active site: Cys (phosphocysteine intermediate) #status predicted
F:263/Binding site: substrate phosphate (Arg) #status predicted

Query Match 88.5%; Score 46; DB 1; Length 314;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCAGISRS 10
||| |||||
Db 255 VHCAGISRS 264

RESULT 12
B57126
Dual specificity phosphatase (EC 3.1.3.-) 2 - mouse
N:Alternate names: mitogen-induced nuclear protein-tyrosine-phosphatase PAC-1
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 24-Apr-1998
C:Accession: B57126
R:Rohan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Kruttsch, H.; Siebenlist, U.; Kel, Science 259, 1763-1766, 1993
A:Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
A:Reference number: A57126; MUID:93206122; PMID:7681221
A:Accession: B57126
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-314 <ROH>
A:Cross-references: GB:L11330
C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity C:Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase

F:180-311/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
 F:257/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:263/Binding site: substrate phosphate (Arg) #status predicted

Query Match 88.5%; Score 46; DB 2; Length 314;
 Best Local Similarity 90.0%; Pred. No. 0.27;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 ||| |||||
 Db 255 VHCQAGISRS 264

RESULT 13

S29090
 N:Alternate names: dual specificity phosphoprotein phosphatase (EC 3.1.1.3.-) 1 - human
 C:Species: Homo sapiens (man)
 C:Date: 25-Feb-1994 #sequence_revision 02-May-1994 #text_change 11-Jun-1999
 C:Accession: S29090; A53052
 R:Keyse, S.M.; Emslie, E.A.
 Nature 359, 644-647, 1992
 A:Title: Oxidative stress and heat shock induce a human gene encoding a protein-tyrosine phosphatase
 A:Reference number: S29090; MUID:93024952; PMID:1406996
 A:Accession: S29090
 A:Molecule type: mRNA
 A:Residues: 1-367 <KEY>
 A:Cross-references: EMBL:X68277; NID:g29980; PIDN:CAA48338.1; PID:g29981
 R:Kwak, S.P.; Hakes, D.J.; Martell, K.J.; Dixon, J.E.
 J. Biol. Chem. 269, 3596-3604, 1994
 A:Title: Isolation and characterization of a human dual specificity protein-tyrosine phosphatase cDNA
 A:Reference number: A53052; MUID:94148864; PMID:8106404
 A:Accession: A53052
 A:Molecule type: DNA
 A:Residues: 1-367 <KWA>
 A:Experimental source: leukocyte
 A:Note: sequence extracted from NCBI backbone (NCBIN:143800, NCBIN:143802, NCBIN:143804, NCBIN:143806)

C:Genetics:
 A:Gene: GDB:DUSP1; PTPN10
 A:Cross-references: GDB:136197; OMIM:600714
 A:Map position: 5q34-5q34
 C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity phosphoprotein phosphatase 1; phosphoric monoester hydrolase; stress-induced phosphatase
 F:181-312/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
 F:258/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:264/Binding site: substrate phosphate (Arg) #status predicted

Query Match 88.5%; Score 46; DB 1; Length 367;
 Best Local Similarity 90.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 ||| |||||
 Db 256 VHCQAGISRS 265

RESULT 14

S24411
 N:Alternate names: 3CHL34 protein; protein-tyrosine-phosphatase erp, nonreceptor type 10
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Feb-1994 #sequence_revision 02-May-1994 #text_change 11-Jun-1999
 C:Accession: A54681; S24411
 R:Noguchi, T.; Metz, R.; Chen, L.; Mattei, M.G.; Carrasco, D.; Bravo, R.
 Mol. Cell. Biol. 13, 5195-5205, 1993
 A:Title: Structure, mapping, and expression of erp, a growth factor-inducible gene encoded by the mouse genome
 A:Reference number: A54681; MUID:93360956; PMID:8355678
 A:Accession: A54681
 A:Molecule type: DNA
 A:Residues: 1-367 <NOG>
 A:Cross-references: GB:S64851; NID:g409976; PIDN:AAB27882.1; PID:g409977
 R:Charles, C.H.; Abler, A.S.; Lau, L.F.
 Oncogene 7, 187-190, 1992

Query Match 88.5%; Score 46; DB 2; Length 367;
 Best Local Similarity 90.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 ||| |||||
 Db 256 VHCQAGISRS 265

Search completed: September 23, 2004, 14:21:35
 Job time : 24 secs

A:Title: cDNA sequence of a growth factor-inducible immediate early gene and character of its protein product
 A:Reference number: S24411; MUID:92158357; PMID:1741163
 A:Accession: S24411
 A:Molecule type: mRNA
 A:Residues: 1-367 <CHNA>
 A:Cross-references: EMBL:X61940; NID:g49735; PIDN:CAA43944.1; PID:g49736
 C:Genetics:
 A:Gene: erp
 A:Introns: 123/1; 172/1; 245/1
 C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity phosphoprotein phosphatase 1; phosphoric monoester hydrolase
 F:181-312/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
 F:258/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:264/Binding site: substrate phosphate (Arg) #status predicted

Query Match 88.5%; Score 46; DB 1; Length 367;
 Best Local Similarity 90.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 ||| |||||
 Db 256 VHCQAGISRS 265

RESULT 15

S52265
 N:Alternate names: dual specificity phosphatase (EC 3.1.1.3.-) 1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 22-Jun-1999
 C:Accession: S52265
 R:Muda, M.; Schlegel, W.; Arkinstall, S.
 submitted to the EMBL Data Library, January 1995
 A:Description: Pathways regulating CL100 gene expression in pituitary cells.
 A:Reference number: S52265
 A:Accession: S52265
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-367 <MUD>
 A:Cross-references: EMBL:X84004; NID:g642264; PIDN:CAA58828.1; PID:g642265
 C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity phosphoprotein phosphatase 1; phosphoric monoester hydrolase
 F:181-312/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
 F:258/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:264/Binding site: substrate phosphate (Arg) #status predicted

Query Match 88.5%; Score 46; DB 2; Length 367;
 Best Local Similarity 90.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 ||| |||||
 Db 256 VHCQAGISRS 265

protein - protein search, using sw model

on: September 23, 2004, 14:18:58 ; Search time 10 Seconds
(without alignments)
52.070 Million cell updates/sec

file: US-09-964-277-16

fect score: 52

quence: 1 VHCLAGISRS 10

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 141681 seqs, 52070155 residues

tal number of hits satisfying chosen parameters: 141681

imum DB seq length: 0

imum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : SwissProt_42:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	52	100.0	276	PTP3 CHLEU	Q39491 chlamydomon
2	52	100.0	280	DUSP RAT	Q63340 rattus norv
3	52	100.0	320	DUS7 HUMAN	Q16829 homo sapien
4	52	100.0	320	DUS7 MOUSE	Q91246 mus musculu
5	52	100.0	381	DUS6 HUMAN	Q16828 homo sapien
6	52	100.0	381	DUS6 MOUSE	Q9dbb1 mus musculu
7	52	100.0	381	DUS6 RAT	Q64346 rattus norv
8	52	100.0	625	DUS8 HUMAN	Q13202 homo sapien
9	52	100.0	663	DUS8 MOUSE	Q09112 mus musculu
10	52	100.0	665	DUSG HUMAN	Q9by84 homo sapien
11	51	98.1	384	DUS9 HUMAN	Q99556 homo sapien
12	51	98.1	619	VHPI CAEEL	Q10038 caenorhabdi
13	48	92.3	125	DUSF MOUSE	Q8r4v2 mus musculu
14	48	92.3	295	DUSF HUMAN	Q9hir2 homo sapien
15	47	90.4	166	DUSP FOWPV	Q9j592 fowlpox vir
16	46	88.5	178	DUSP MYXVL	Q85297 myxoma viru
17	46	88.5	198	DUSE HUMAN	Q95147 homo sapien
18	46	88.5	198	DUSE MOUSE	Q9jly7 mus musculu
19	46	88.5	314	DUS2 HUMAN	Q05923 homo sapien
20	46	88.5	318	DUS2 MOUSE	Q05922 mus musculu
21	46	88.5	367	DUS1 HUMAN	P28562 homo sapien
22	46	88.5	367	DUS1 MOUSE	P28563 mus musculu
23	46	88.5	367	DUS1 RAT	Q64623 rattus norv
24	46	88.5	375	DUS4 CHICK	Q9pw71 gallus gall
25	46	88.5	375	DUS4 HUMAN	Q13115 homo sapien
26	46	88.5	395	DUS4 RAT	Q62767 rattus norv
27	45	86.5	171	DUSP VARV	P33064 variola vir
28	45	86.5	384	DUS5 HUMAN	Q16690 homo sapien
29	45	86.5	807	YB9T YEAST	P38148 saccharomyc
30	44	84.6	339	DUSC MOUSE	Q9d0r2 mus musculu
31	44	84.6	340	DUSC HUMAN	Q9uni6 homo sapien
32	44	84.6	384	DUS5 RAT	O54818 rattus norv
33	44	84.6	482	DUSA_HUMAN	Q9y6w6 homo sapien

34	44	84.6	483	1	DUSA_MOUSE	Q9ess0 mus musculu
35	43	82.7	171	1	DUSP_VACCC	P20495 vaccinia vi
36	43	82.7	171	1	DUSF_VACCV	P07239 vaccinia vi
37	43	82.7	171	1	VH01_RACVI	P80994 raccoon pox
38	43	82.7	188	1	DUSI_HUMAN	Q8neJ0 homo sapien
39	42	80.8	160	1	PTP2_NPPOP	O10273 orgyia pseu
40	42	80.8	377	1	PTP2_DICDI	P34138 dictyosteli
41	42	80.8	432	1	PTN1_MOUSE	P35821 mus musculu
42	42	80.8	432	1	PTN1_RAT	P20417 rattus norv
43	42	80.8	434	1	PTN1_CHICK	O13016 gallus gall
44	42	80.8	435	1	PTN1_HUMAN	P18031 homo sapien
45	42	80.8	989	1	PTP3_DICDI	P54637 dictyosteli

ALIGNMENTS

RESULT 1

ID	PTP3 CHLEU	STANDARD;	PRT;	276 AA.
AC	Q39491;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Dual specificity protein phosphatase (EC 3.1.3.48) (EC 3.1.3.16).			
GN	VH-PTP13.			
OS	Chlamydomonas eugametos.			
OC	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;			
OC	Chlamydomonadaceae; Chlamydomonas.			
OX	NCBI_taxID=3053;			
RN	[1]			
RP	SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS OF CYS-172.			
RC	STRAIN=UTEX 10;			
RX	MEDLINE=95323001; PubMed=7599654;			
RA	Haring M.A., Siderius M., Jonak C., Hirt H., Walton K.M.,			
RA	Musgrave A.;			
RT	"Tyrosine phosphatase signalling in a lower plant: cell-cycle and			
RT	oxidative stress-regulated expression of the Chlamydomonas eugametos			
RT	VH-PTP13 gene.";			
RL	Plant J. 7:981-988(1995).			
CC	-!- FUNCTION: Could be involved in tyrosine phosphatase signalling			
CC	pathways, having MAP-kinases as substrates.			
CC	-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein			
CC	tyrosine + phosphate.			
CC	-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +			
CC	phosphate.			
CC	-!- DEVELOPMENTAL STAGE: Nondividing gametes did not express the VH-			
CC	PTP13 gene whereas synchronously dividing vegetative cells only			
CC	expressed VH-PTP13 in the early G1-phase of the cycle.			
CC	-!- INDUCTION: By oxidative stress.			
CC	-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.			
CC	Non-receptor class dual specificity subfamily.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; X77938; CAA54910.1; --			
DR	PIR; T4B906; T4B906.			
DR	HSSP; P51452; 1VHR.			
DR	InterPro; IPR000340; DS_phosphatase.			
DR	InterPro; IPR000387; TYR_phosphatase.			
DR	Pfam; PF00782; DSPC; 1			
DR	SMART; SM00195; DSPC; 1			
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.			
DR	PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.			
KW	Hydrolase.			
FT	DOMAIN 89 276 CATALYTIC.			

FT ACT SITE 172 172 PHOSPHOCYSTEINE INTERMEDIATE.
 FT MUTAGEN 172 172 C-S: COMPLETE LOSS OF ACTIVITY.
 SQ SEQUENCE 276 AA; 30310 MW; 034EF3951E03381 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 276;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 DB 170 VHCLAGISRS 179

RESULT 2
 DUST7 RAT STANDARD; PRT; 280 AA.
 AC Q63340;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dual specificity protein phosphatase 7 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Dual specificity protein phosphatase MKP-X) (Fragment).
 GN DUSP7 OR MKPX.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Neuron;
 RX MEDLINE=96224012; PubMed=8626780;
 RA Muda M., Boschart U., Dickinson R., Martinou J.C., Martinou I.,
 RA Camps M., Schlegel W., Arkinstall S.;
 RT "MKP-3, a novel cytosolic protein-tyrosine phosphatase that
 RT exemplifies a new class of mitogen-activated protein kinase
 RT phosphatase.";
 RL J. Biol. Chem. 271:4319-4326(1996).
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class dual specificity subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X94186; CAA63896.1; -;
 DR HSP; Q16828; 1MKP.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR008343; MAPK_phosph.
 DR Pfam; PF00782; DSPC; 1.
 DR PRINTS; PR01764; MAPKPHPTASE.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00554; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase.
 FT NON TER 1
 FT DOMAIN 169 237 PROTEIN-TYROSINE PHOSPHATASE. (BY
 FT ACT_SITE 192 192 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT SIMILARITY).
 SQ SEQUENCE 280 AA; 30668 MW; 45D6F4A92F2BBDDF CRC64;

Query Match 100.0%; Score 52; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 DB 170 VHCLAGISRS 179

RESULT 3
 DUST7 HUMAN STANDARD; PRT; 320 AA.
 AC Q16829;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dual specificity protein phosphatase 7 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Dual specificity protein phosphatase PYST2).
 GN DUSP7 OR PYST2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=96312959; PubMed=8670865;
 RA Groom L.A., Sneddon A.A., Alessi D.R., Dowd S., Keyse S.M.;
 RT "Differential regulation of the MAP, SAP and RK/p38 kinases by Pyst1,
 RT a novel cytosolic dual-specificity phosphatase.";
 RL EMBO J. 15:3621-3632(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class dual specificity subfamily.
 CC -----
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 CC -----
 CC EMBL; X93921; CAA63814.1; ALT_INIT.
 DR EMBL; X93921; CAA63814.1; ALT_INIT.
 DR HSP; Q16828; 1MKP.

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 DB 190 VHCLAGISRS 199

RESULT 3
 DUST7 HUMAN STANDARD; PRT; 320 AA.
 AC Q16829;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dual specificity protein phosphatase 7 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Dual specificity protein phosphatase PYST2).
 GN DUSP7 OR PYST2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=96312959; PubMed=8670865;
 RA Groom L.A., Sneddon A.A., Alessi D.R., Dowd S., Keyse S.M.;
 RT "Differential regulation of the MAP, SAP and RK/p38 kinases by Pyst1,
 RT a novel cytosolic dual-specificity phosphatase.";
 RL EMBO J. 15:3621-3632(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class dual specificity subfamily.
 CC -----
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 CC -----
 CC EMBL; X93921; CAA63814.1; ALT_INIT.
 DR EMBL; X93921; CAA63814.1; ALT_INIT.
 DR HSP; Q16828; 1MKP.

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CC -----

DR EMBL; BC010207; AAH10207.1; -
DR MGD; MGI:2387100; Dusp7.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR008343; MAPK_phosph.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR PRINTS; PR01764; MAPKPHPTASE.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
XW Hydrolase.
FT DOMAIN 209 277 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 232 232 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT ACT_SITE 232 232 SIMILARITY).
SQ SEQUENCE 320 AA; 35258 MW; 2AAD2723E27DAE53 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | | | |
DB 230 VHCLAGISRS 239

RESULT 5
DUS6 HUMAN STANDARD; PRT; 381 AA.
ID Q1828; O75109; Q9BSH6;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dual specificity protein kinase phosphatase 6 (EC 3.1.3.48) (EC 3.1.3.16)
DE (Mitogen-activated protein kinase phosphatase 3) (MAP kinase PYS1).
DE phosphatase 3) (MKP-3) (Dual specificity protein phosphatase PYS1).
DE DUSP6 OR MKP3 OR PYS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Forebrain;
RX MEDLINE=96312959; PubMed=8670865;
RA Groom L.A., Sneddon A.A., Alessi D.R., Dowd S., Keyse S.M.,
RT "Differential regulation of the MAP, SAP and RK/p38 kinases by Pys1,
RL a novel cytosolic dual-specificity phosphatase.";
RL EMBO J. 15:3621-3632(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Liver;
RX MEDLINE=93077745; PubMed=9658808;
RA Furukawa T., Yatsuka T., Youssef E.M., Abe T., Yokoyama T.,
RA Fukushima S., Soeda E., Hoshi M., Hayaishi Y., Sunamura M., Kobari M.,
RA Horii A.;
RT "Genomic analysis of DUSP6, a dual specificity MAP kinase phosphatase,
RL in pancreatic cancer.";
RL Cytogenet. Cell Genet. 82:156-159(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT VAL-114.
RC TISSUE=Colon, Kidney, Skin, and Stomach;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

2 MIM: 602749; -
2 GO: GO:0005737; C:cytoplasm; ISS.
2 GO: GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
2 GO: GO:0004725; F:protein tyrosine phosphatase activity; ISS.
2 GO: GO:0000188; P:inactivation of MAPK; ISS.
2 InterPro; IPR000340; DS_phosphatase.
2 InterPro; IPR008343; MAPK_phosph.
2 InterPro; IPR000387; TYR_phosphatase.
2 Pfam; PF00782; DSPC; 1.
2 PRINTS; PR01764; MAPKPHPTASE.
2 SMART; SM00195; DSPC; 1.
2 PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
2 PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
2 PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.

4 Hydrolase.
FT DOMAIN 209 277 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 232 232 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT ACT_SITE 232 232 SIMILARITY).
SQ SEQUENCE 320 AA; 35278 MW; D387F6BFBFA92113C CRC64;

Query Match 100.0%; Score 52; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VHCLAGISRS 10
| | | | | | | | | |
D 230 VHCLAGISRS 239

RESULT 4
US7 MOUSE STANDARD; PRT; 320 AA.
C Q91Z46;
I 28-FEB-2003 (Rel. 41, Created)
I 28-FEB-2003 (Rel. 41, Last sequence update)
I 10-OCT-2003 (Rel. 42, Last annotation update)
E Dual specificity protein phosphatase 7 (EC 3.1.3.48) (EC 3.1.3.16).
N DUSP7.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
X MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalusz D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
IT "Generation and initial analysis of more than 15,000 full-length
IT human and mouse cDNA sequences.";
IL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
C -I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
C tyrosine + phosphate.
C -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
C phosphate.
C -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
C -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
C Non-receptor class dual specificity subfamily.
C -----

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Icoquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 204-347.
RX MEDLINE=99140299; PubMed=10048930;
RA Stewart A.E., Dowd S., Keyse S.W., McDonald N.Q.;
RT "Crystal structure of the MAPK phosphatase Pyst1 catalytic domain and
RT implications for regulated activation";
RL Nat. Struct. Biol. 6:174-181(1999).
CC -I- FUNCTION: Inactivates MAP kinases. Has a specificity for the ERK
CC family.
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q16828-1; Sequence=Displayed;
CC Name=2; Synonyms=DUSP6-ALT;
CC IsoId=Q16828-2; Sequence=VSP_005137;
CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class dual specificity subfamily.
CC -I- SIMILARITY: Contains 1 rhodanese domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X93920; CAA63813.1; -;
DR EMBL; AB013601; BAA31968.1; -;
DR EMBL; AB013383; BAA31968.1; JOINED.
DR EMBL; AB013600; BAA31968.1; JOINED.
DR EMBL; AB013382; BAA3369.1; -;
DR EMBL; AB013602; BAA31969.1; -;
DR EMBL; BC003143; AAH03143.1; -;
DR EMBL; BC003562; AAH03562.1; -;
DR EMBL; BC005047; AAH05047.1; -;
DR EMBL; BC037236; AAH37236.1; -;
DR FDB; IMKP; 22-JUL-99.
DR PDB; 1HZM; 25-JAN-02.
DR Genew; HGNC:3072; DUSP6.
DR MIM; 602748; -;
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IDA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IDA.
DR GO; GO:0000188; P:inactivation of MAPK; IDA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR008343; MAPK_phosph.
DR InterPro; IPR001763; Rhodanese-like

DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR Pfam; PF00581; Rhodanese; 1.
DR PRINTS; PR01764; MAPKPHPTASE.
DR SMART; SM00195; DSPC; 1.
DR SMART; SM00450; RHOD; 1.
DR PROSITE; PS00206; RHODANESE 3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; FALSE_NEG.
DR PROSITE; PS00556; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00554; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase; Polymorphism; Alternative splicing; 3D-structure.
FT DOMAIN 30 148
FT RHODANESE.
FT DOMAIN 206 381
FT PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 233 293
FT PHOSPHOCYSTEINE INTERMEDIATE.
FT VARSPLIC 134 279
FT Missing (in isoform 2).
FT /FTID=VSP_005137.
FT L -> V.
FT /FTID=VAR_015113.

FT STRAND 208 211
FT TURN 212 213
FT STRAND 214 217
FT TURN 219 220
FT TURN 220 220
FT HELIX 225 230
FT TURN 231 232
FT TURN 231 232
FT STRAND 233 238
FT STRAND 246 250
FT TURN 251 252
FT STRAND 253 257
FT TURN 264 265
FT TURN 269 271
FT HELIX 272 284
FT TURN 285 286
FT STRAND 288 292
FT HELIX 298 312
FT TURN 313 313
FT HELIX 316 326
FT TURN 328 329
FT TURN 335 336
FT HELIX 337 345
FT TURN 346 346
SQ SEQUENCE 381 AA; 42333 MW; 03BC12252CE73B26 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | | | |
Db 291 VHCLAGISRS 300

RESULT 6

ID DUSE_MOUSE STANDARD; PRT; 381 AA.
AC Q9DBB1; Q9D7L4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dual specificity protein phosphatase 6 (EC 3.1.3.48) (EC 3.1.3.16)
DE (Mitogen-activated protein kinase phosphatase 3) (MAP kinase
DE phosphatase 3) (MKP-3).
GN DUSP6 OR MKP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STAIN-C57BL/6J; TISSUE=Liver, and Tongue;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka T.
RN

A Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
A Kuehl P., Lewis S., Matsuo Y., Nitaide I., Resole G., Quackenbush J.,
A Sakurai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
A Blake J., Boffelli D., Bojunga R., Carninci P., de Bonaldo M.P.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
A Hayashizaki Y.;
I "Functional annotation of a full-length mouse cDNA collection.";
L Nature 409:685-690(2001).
N [2]
P SEQUENCE FROM N.A.
X MEDLINE-22388257; PubMed-12477932;
A Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.W., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
A Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
I "Generation and initial analysis of more than 15,000 full-length
L human and mouse cDNA sequences.";
P Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
X -!- FUNCTION: Inactivates MAP kinases. Has a specificity for the ERK
family (By similarity).
C -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
C tyrosine + phosphate.
C -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
C phosphate.
C -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
C -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
C -!- SIMILARITY: Contains 1 rhodanese domain.
C -----
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C or send an email to license@sib-sib.ch).
C -----
C R EMBL; AK005062; BAB23786.1; -;
C R EMBL; AK009131; BAB26093.1; -;
C R EMBL; BC003869; AAH03869.1; -;
C R HSP; Q16828; 1MKP.
C R MGD; MG1:1914853; Dusp6.
C R InterPro; IPR000340; DS_phosphatase.
C R InterPro; IPR008343; MAPK_phosph.
C R InterPro; IPR001763; Rhodanese-like.
C R InterPro; IPR000387; TYR_phosphatase.
C R Pfam; PF00782; DSPC; 1.
C R PRINTS; PR01764; MAPKPHPTASE.
C R SMART; SM00195; DSPC; 1.
C R SMART; SM00450; RHOD; 1.
C R PROSITE; PS50206; RHODANESE_3; 1.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase.
FT DOMAIN 30 148 RHODANESE.
FT DOMAIN 206 381 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 293 293 PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT CONFLICT 22 22 W -> G (IN REF. 1; BAB26093).
FT CONFLICT 34 34 L -> F (IN REF. 1; BAB26093).
SQ SEQUENCE 381 AA; 42407 MW; 7EA1F154F4AD2DA CRC64;
Query Match 100.0%; Score 52; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VHLGAGISRS 10
| | | | | | | | | |
DB 291 VHLGAGISRS 300
RESULT 7
DUS6 RAT
ID DUS6 RAT STANDARD; PRT; 381 AA.
AC Q64346.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dual specificity protein phosphatase 6 (EC 3.1.3.48) (EC 3.1.3.16)
DE Mitogen-activated protein kinase phosphatase 3 (MAP kinase
DE phosphatase 3) (MKP-3).
DE DUSP6 OR MKP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-Sprague-Dawley; TISSUE=Neuron;
RX MEDLINE=96224012; PubMed=8626780;
RA Muda M., Boschert U., Dickinson R., Martinou J.C., Martinou I.,
RA Camps M., Schlegel W., Arkinstall S.;
RT "MKP-3, a novel cytosolic protein-tyrosine phosphatase that
RT exemplifies a new class of mitogen-activated protein kinase
RT phosphatase.";
RL J. Biol. Chem. 271:4319-4326(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96216487; PubMed=8631996;
RA Mourey R.J., Vega Q.C., Campbell J.S., Wenderoth M.P., Hauschka S.D.,
RA Krebs E.G., Dixon J.E.;
RT "A novel cytoplasmic dual specificity protein tyrosine phosphatase
RT implicated in muscle and neuronal differentiation.";
RL J. Biol. Chem. 271:3795-3802(1996).
CC -!- FUNCTION: Inactivates MAP kinases. Has a specificity for the ERK
family. Implicated in muscle and neuronal differentiation.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -!- SIMILARITY: Contains 1 rhodanese domain.
CC -----
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DR EMBL; X94185; CAAC3895.1; -.
DR EMBL; U42627; AAB06202.1; -.
DR HSP; Q16828; 1MKP.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR008343; MAPK_phosph.
DR InterPro; IPR001763; Rhodanese-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR Pfam; PF00581; Rhodanese; 1.
DR PRINTS; PR01764; MAPKPHPTASE.
DR SMART; SM00195; DSPC; 1.
DR SMART; SM00450; RHOD; 1.
DR PROSITE; PS50206; RHODANESE_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase.
FT DOMAIN 30 148 RHODANESE.
FT DOMAIN 206 381 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 293 293 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
SQ SEQUENCE 381 AA; 42318 MW; C511E00CB68F2888 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
DB 291 VHCLAGISRS 300
|||||

RESULT 8
DUS8_HUMAN
ID DUS8_HUMAN STANDARD; PRT; 625 AA.
AC Q13202;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Dual specificity protein phosphatase 8 (EC 3.1.3.48) (RC 3.1.3.16)
DE (Dual specificity protein phosphatase hVH-5).
GN DUSP8 OR VHS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=96009533; PubMed=7561881;
RA Martell K.J., Seasholtz A.F., Kwak S.P., Clemens K.K., Dixon J.E.;
RT "hVH-5: a protein tyrosine phosphatase abundant in brain that
inactivates mitogen-activated protein kinase.";
RL J. Neurochem. 65:1823-1833(1995).
CC -!- FUNCTION: This protein shows both activity toward tyrosine-protein
phosphate as well as with serine/threonine-protein phosphate (By
similarity).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -!- TISSUE SPECIFICITY: Abundant in brain, heart and skeletal muscle.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -!- Non-receptor class dual specificity subfamily.
CC -!- SIMILARITY: Contains 1 rhodanese domain.
-----
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CC EMBL; U27193; AAA83151.1; -.
CC HSP; Q16828; 1MKP.
CC Genew; HGNC:3074; DUSP8.
CC MIM; 602038; -.
CC GO; GO:0005737; C:cytoplasm; TAS.
CC GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS.
CC GO; GO:0001188; P:inactivation of MAPK; TAS.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC InterPro; IPR000340; DS_phosphatase.
CC InterPro; IPR008343; MAPK_phosph.
CC InterPro; IPR001763; Rhodanese-like.
CC InterPro; IPR000387; TYR_phosphatase.
CC Pfam; PF00782; DSPC; 1.
CC PRINTS; PR01764; MAPKPHPTASE.
CC SMART; SM00195; DSPC; 1.
CC SMART; SM00450; RHOD; 1.
CC PROSITE; PS50206; RHODANESE_3; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase; Nuclear protein.
FT DOMAIN 23 138 RHODANESE.
FT DOMAIN 162 430 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 310 550 PRO-RICH.
FT ACT_SITE 246 246 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
SQ SEQUENCE 625 AA; 65840 MW; DCBEAL487219666 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 625;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
DB 244 VHCLAGISRS 253
|||||

RESULT 9
DUS8_MOUSE
ID DUS8_MOUSE STANDARD; PRT; 663 AA.
AC Q09112;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dual specificity protein phosphatase 8 (EC 3.1.3.48) (RC 3.1.3.16)
DE (Neuronal tyrosine threonine phosphatase 1).
GN DUSP8 OR NTP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96311565; PubMed=8733137;
RA Theodosiou A.M., Rodrigues N.R., Nesbit M.A., Ambrose H.J.,
RA Paterson H., McEllan-Arnold E., Boyd Y., Leversha M.A., Owen N.,
RA Blake D.J., Ashworth A., Davies K.E.;
RT "A member of the MAP kinase phosphatase gene family in mouse
containing a complex trinucleotide repeat in the coding region.";
RL Hum. Mol. Genet. 5:675-684(1996).
CC -!- FUNCTION: This protein shows both activity toward tyrosine-protein
phosphate as well as with serine/threonine-protein phosphate (By
similarity).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- TISSUE SPECIFICITY: Expressed predominantly in brain and lung.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -!- Non-receptor class dual specificity subfamily.

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C  -!- SIMILARITY: Contains 1 rhodanese domain.
C  -----
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C  entities requires a license agreement (See http://www.isb-sib.ch/announce/
C  or send an email to license@isb-sib.ch).
C  -----
C  EMBL; X95518; CAAG4772.1; --
C  HSSP; Q16828; IMKP.
C  R  MGI; 106626; Dusp8.
C  R  InterPro; IPR000340; DS_phosphatase.
C  R  InterPro; IPR008343; MAPK_phosph.
C  R  InterPro; IPR001763; Rhodanese-like.
C  R  InterPro; IPR000387; TYR_phosphatase.
C  R  Pfam; PF00782; DSPC; 1.
C  R  PRINTS; PR01764; MAPKPHPTASE.
C  R  SMART; SM00195; DSPC; 1.
C  R  SMART; SM00450; RHOD; 1.
C  R  PROSITE; PS50206; RHODANESE_3; 1.
C  R  PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
C  R  PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
C  R  PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
C  W  Hydrolase; Nuclear protein.
C  T  DOMAIN 23 138 RHODANESE.
C  T  DOMAIN 162 432 PROTEIN-TYROSINE PHOSPHATASE.
C  T  DOMAIN 452 459 POLY-ARG.
C  T  DOMAIN 555 558 POLY-SER.
C  T  DOMAIN 559 576 POLY-GLY.
C  T  DOMAIN 577 600 POLY-SER.
C  T  DOMAIN 311 552 PRO-RICH.
C  T  DOMAIN 246 246 PHOSPHOCYSTEINE INTERMEDIATE (BY
C  T  ACT_SITE SIMILARITY).
C  T  SEQUENCE 663 AA; 68847 MW; 416F429A12C1FA7C CRC64;
C  Query Match 100.0%; Score 52; DB 1; Length 663;
C  Best Local Similarity 100.0%; Pred. No. 0.013;
C  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y  1 VHCLAGISRS 10
b  244 VHCLAGISRS 253
-----
ESULT 10
USG HUMAN STANDARD; PRT; 665 AA.
C  Q9BY84; Q9CGG3;
C  28-FEB-2003 (Rel. 41, Created)
C  28-FEB-2003 (Rel. 41, Last sequence update)
C  10-OCT-2003 (Rel. 42, Last annotation update)
E  Dual specificity protein phosphatase 16 (EC 3.1.3.48) (EC 3.1.3.16)
E  (Mitogen-activated protein kinase phosphatase 7) (MAP kinase
E  phosphatase 7) (MKP-7).
E  DUSP16 OR MKP7 OR KIAA1700.
S  Homo sapiens (Human).
C  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X  NCBI_TaxID=9606;
X  [1]
P  SEQUENCE FROM N.A.
X  MEDLINE=21486429; PubMed=11489891;
X  Masuda K., Shima H., Watanabe M., Kikuchi K.;
T  "MKP-7, a novel mitogen-activated protein kinase phosphatase,
T  functions as a shuttle protein."
L  J. Biol. Chem. 276:39002-39011(2001).
L  [2]
N  SEQUENCE FROM N.A.
P  TISSUE=Brain;
X  MEDLINE=21082932; PubMed=11214970;
X  Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;

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RT  *Prediction of the coding sequences of unidentified human genes. XIX.
RT  The complete sequences of 100 new cDNA clones from brain which code
RT  for large proteins in vitro.;
RL  DNA Res. 7:347-355(2000).
CC  -!- FUNCTION: Involved in the inactivation of MAP kinases.
CC  -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC  tyrosine + phosphate.
CC  -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC  phosphate.
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC  -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC  -!- SIMILARITY: Contains 1 rhodanese domain.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; AB052156; BAB40814.1; --
CC  EMBL; AB051487; BAB21791.1; ALT_INIT.
CC  HSSP; Q16828; IMKP.
CC  Genew; HGNC:17909; DUSP16.
CC  MIM; 607175; --
CC  GO; GO:0005737; Cytoplasm; TAS.
CC  GO; GO:0005634; C:nucleus; TAS.
CC  GO; GO:0004721; P:protein phosphatase activity; TAS.
CC  GO; GO:0016311; P:dephosphorylation; TAS.
CC  GO; GO:0000188; P:inactivation of MAPK; TAS.
CC  GO; GO:0045209; P:leptomycin B-sensitive MAPK phosphatase nuc. . .; TAS.
CC  GO; GO:0045204; P:MAPK nucleus export; TAS.
CC  InterPro; IPR000340; DS_phosphatase.
CC  InterPro; IPR008343; MAPK_phosph.
CC  InterPro; IPR000387; TYR_phosphatase.
CC  Pfam; PF00782; DSPC; 1.
CC  Pfam; PF00581; Rhodanese; 1.
CC  PRINTS; PR01764; MAPKPHPTASE.
CC  SMART; SM00195; DSPC; 1.
CC  SMART; SM00450; RHOD; 1.
CC  PROSITE; PS50206; RHODANESE_3; 1.
CC  PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC  PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC  PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
C  W  Hydrolase; Nuclear protein.
C  FT  DOMAIN 22 137 RHODANESE.
C  FT  DOMAIN 227 289 PROTEIN-TYROSINE PHOSPHATASE.
C  FT  ACT_SITE 244 244 PHOSPHOCYSTEINE INTERMEDIATE (BY
C  SIMILARITY).
C  SQ  SEQUENCE 665 AA; 73101 MW; 1BD853FF08460DFF CRC64;
C  Query Match 100.0%; Score 52; DB 1; Length 665;
C  Best Local Similarity 100.0%; Pred. No. 0.013;
C  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q  1 VHCLAGISRS 10
Db  242 VHCLAGISRS 251
-----
RESULT 11
ID  DUSG_HUMAN STANDARD; PRT; 384 AA.
AC  Q99856;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Dual specificity protein phosphatase 9 (EC 3.1.3.48) (EC 3.1.3.16)
DE  (Mitogen-activated protein kinase phosphatase 4) (MKP-4).
DE  phosphatase 4) (MKP-4).

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GN DUSP9 OR MKP4.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97184159; PubMed=9030581;
 RA Mada M., Boschart U., Smith A., Antonsson B., Gyllerion C.,
 RA Chabert C., Camps M., Martinou I., Ashworth A., Arkinstall S.;
 RT "Molecular cloning and functional characterization of a novel
 RT mitogen-activated protein kinase phosphatase, MKP-4.";
 RL J. Biol. Chem. 272:5141-5151(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Platzer M.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: Inactivates MAP kinases. Has a specificity for the ERK
 CC family.
 CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC -I- SIMILARITY: Contains 1 rhodanese domain.
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 CC
 DR EMBL; Y08302; CAA69610.1; -;
 DR EMBL; U52111; -; NOT_ANNOTATED_CDS.
 DR HSP; Q16828; IMKP.
 DR Genew; HGNC:3076; DUSP9.
 DR MIM; 300134; -;
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0004721; P:protein phosphatase activity; TAS.
 DR GO; GO:0001188; P:inactivation of MAPK; TAS.
 DR GO; GO:0007254; P:JNK cascade; TAS.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR008343; MAPK_phosph.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR PRINTS; PR01764; MAPKPHPTASE.
 DR SMART; SM00195; DSPC; 1.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS0206; RHODANASE_3; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase.
 FT DOMAIN 18 139 RHODANASE.
 FT DOMAIN 203 384 PROTEIN-TYROSINE PHOSPHATASE
 FT ACT_SITE 290 290 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT SIMILARITY).
 SQ SEQUENCE 384 AA; 41867 MW; F8598CA95AB379B7 CRC64;
 Query Match 98.1%; Score 51; DB 1; Length 384;
 Best Local Similarity 90.0%; Pred. No. 0.012; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHLAGISRS 10
 |||||:||||

DB 288 VHLAGVRS 297
 RESULT 12
 VHPI_CAEEL
 ID VHPI_CAEEL STANDARD; PRT; 619 AA.
 AC Q10038;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase vhp-1 (EC 3.1.3.48).
 GN VHP-1 OR F08B1.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Telodermata; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Chisoe S.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC -I- SIMILARITY: Non-receptor class dual specificity subfamily.
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 CC
 DR EMBL; U23178; AAC46719.1; -;
 DR PIR; T15969; T15969.
 DR HSP; Q16828; IMKP.
 DR WormPep; F08B1.1; CE01899.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase.
 FT DOMAIN 200 269 PROTEIN-TYROSINE PHOSPHATASE.
 FT DOMAIN 92 95 POLY-SER.
 FT DOMAIN 351 354 POLY-SER.
 FT DOMAIN 465 472 POLY-SER.
 FT DOMAIN 483 488 POLY-SER.
 FT ACT_SITE 224 224 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT SIMILARITY).
 SQ SEQUENCE 619 AA; 66354 MW; 369E326F615D0529 CRC64;
 Query Match 98.1%; Score 51; DB 1; Length 619;
 Best Local Similarity 90.0%; Pred. No. 0.02; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHLAGISRS 10
 :|||||
 DB 222 IHCLAGISRS 231
 RESULT 13
 DUSF_MOUSE
 ID DUSF_MOUSE STANDARD; PRT; 125 AA.
 AC Q8R4V2;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dual specificity protein phosphatase 15 (EC 3.1.3.48) (Fragment).
 DE Dual specificity protein phosphatase T-DSP10 (Fragment).
 DE

N 4. DUSP15.
S. Mus musculus (Mouse).
C. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
M. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
N NCBI_TaxID=10090;
P SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
K MEDLINE=21326039; PubMed=11432789;
A Aoki N., Aoyama K., Nagata M., Matsuda T.;
I "A growing family of dual specificity phosphatases with low molecular
T masses";
J. Biochem. 130:133-140(2001).
N [2]
P SEQUENCE FROM N.A. (ISOFORM 1).
K MEDLINE=21671825; PubMed=11412828;
A Mu X., Zhao S., Pershad R., Hsieh T.-P., Scarpa A., Wang S.W.,
T White R.A., Barendse P.D., Thomas T.L., Gan L., Klein W.H.;
I "Gene expression in the developing mouse retina by EST sequencing and
T microarray analysis";
Nucleic Acids Res. 29:4983-4993(2001).
C -!- CATALYTIC ACTIVITY: protein tyrosine phosphate + H(2)O = protein +
C tyrosine + phosphate.
C -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
C phosphate.
C -!- ALTERNATIVE PRODUCTS:
C Event=Alternative splicing; Named isoforms=2;
C Name=1;
C IsoId=Q8RAV2-1; Sequence=Displayed;
C Note=Derived from EST data;
C Name=2;
C IsoId=Q8RAV2-2; Sequence=VSP_007294, VSP_007295;
C Note=Inactive. Lacks the active site;
C -!- TISSUE SPECIFICITY: Isoform 2 is highly expressed in testis.
C -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
C Non-receptor class dual specificity subfamily.
C -----
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C or send an email to license@isb-sib.ch).
C -----
R EMBL; AF357887; AM00226.1; -;
R EMBL; BU924460; -; NOT_ANNOTATED_CDS.
R MGI; MG1:1934928; Dusp15.
R InterPro: IPR000340; DS_phosphatase.
R InterPro: IPR000387; TYR_phosphatase.
R Pfam; PF00782; DSRc; 1.
R SMART; SM00195; DSRc; 1.
R PROSITE; P500383; TYR_PHOSPHATASE_1; 1.
R PROSITE; P500056; TYR_PHOSPHATASE_2; 1.
R PROSITE; P500054; TYR_PHOSPHATASE_DUAL; 1.
W Hydrolase; Alternative splicing.
T DOMAIN 65 >125 PROTEIN-TYROSINE PHOSPHATASE.
T ACT_SITE 88 88 PHOSPHOCYSTEINE INTERMEDIATE (BY
T SIMILARITY).
T VARSPLIC 88 105 CFAGISRTTIVAYVMT -> WPLKHCARSLSLQCS
T (in isoform 2).
T /FTId=VSP_007294.
T Missing (in isoform 2).
T VARSPLIC 106 125 Missing (in isoform 2).
T /FTId=VSP_007295.
T NON_TER 125 125
T SEQUENCE 125 AA; 13797 MW; D79F87F0120F816 CRC64;
Query Match 92.3%; Score 48; DB 1; Length 125;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1 VHCLAGISRS 10
b |||||
86 VHCFAGISRS 95

RESULT 14
DUSP HUMAN
ID DUSP HUMAN STANDARD; PRT; 295 AA.
AC Q9H1R2; Q9N826; Q9BX24;
DT 28-PEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dual specificity protein phosphatase 15 (EC 3.1.3.48) (EC 3.1.3.16).
GN DUSP15 OR C20ORF57.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A. (ISOFORM 1).
PC TISSUE=Testis;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Magatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RP MEDLINE=21638749; PubMed=11780052;
RX Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Beards K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaealatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLeay D.M., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromane A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20";
RL Nature 414:865-871(2001).
RN [3]
RC SEQUENCE FROM N.A. (ISOFORM 2).
PC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Tashyuk S., Carninci P.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1;

isoId=Q9H1R2-1; Sequence=Displayed;

Name=2;

isoId=Q9H1R2-2; Sequence=VSP_007292, VSP_007293;

Notes=Derived from EST data;

-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Non-receptor class dual specificity subfamily.

-!- CAUTION: Ref.2 sequences differ from that shown due to erroneous gene model prediction.

-!- CAUTION: Although assigned as two separate genes (c20orf57 and DUSP15), it is probable that C20orf57 does not exist by itself and is a part of the DUSP15 gene.

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EMBL; AK097430; BAC05048.1; -;

EMBL; AL160175; CAC10008.2; ALT SEQ.

EMBL; AL160175; CAC28981.1; ALT SEQ.

EMBL; BM554314; -; NOT_ANNOTATED_CDS.

HSSP; P51452; 1VHR.

Genew; HGNC:16236; DUSP15.

Genew; HGNC:16190; C20orf57.

InterPro; IPR000340; DS_phosphatase.

InterPro; IPR000387; TYR_phosphatase.

Pfam; PF00782; DSPC; 1.

SMART; SM00195; DSPC; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

PROSITE; PS00566; TYR_PHOSPHATASE_2; 1.

PROSITE; PS00564; TYR_PHOSPHATASE_DUAL; 1.

Hydrolase; Alternative splicing.

DOMAIN 62 132 PROTEIN-TYROSINE PHOSPHATASE.

ACT_SITE 85 85 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).

VARSPLIC 143 232 GARHRTSKTSGACQPMTSATCLLAARVALLSNAALVREATG RTAQRCLRSFRAARERKLLGPPHHVAGWSGDPKIQICLCFG REDPGTG -> LRRLQLEERFGESPRDEELRALPLCKR CQQGATSASAGPHSAASEGTQRLVPTPTREAHRLPLLR ARVKQTFSCLPRCLSRKGGK (in isoform 2). /FTId=VSP_007292.

VARSPLIC 233 295 Missing (in isoform 2). /FTId=VSP_007293.

SEQUENCE 295 AA; 31881 MW; 28F8A687ECB5C219 CRC64;

Query Match 92.3%; Score 48; DB 1; Length 295;

Best Local Similarity 90.0%; Pred. No. 0.035;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VHLCLAGISRS 10

DB 83 VHCFAGISRS 92

RESULT 15

```

DUSP_FOWPV STANDARD; PRT; 166 AA.
ID DUSP_FOWPV AC Q9J592;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable dual specificity protein phosphatase (EC 3.1.3.48)
DE (EC 3.1.3.16).
GN FFW138.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OC NCBI_TaxID=10261;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=20193820; PubMed=10729156;
AFONSO C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
CC -!- FUNCTION: Shows activity toward tyrosine-protein phosphatase as well
CC as with serine-protein phosphatase (By similarity).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class dual specificity subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF198100; AAF44482.1; -.
CC InterPro; IPR000340; DS_phosphatase.
CC InterPro; IPR00387; TYR_phosphatase.
CC Pfam; PF00782; DSFC; 1.
CC SMART; SM00195; DSPC; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
CC Hydrolyase.
CC ACT_SITE 108 108 PHOSPHOCYSTEINE INTERMEDIATE (BY
CC SIMILARITY).
CC SEQUENCE 166 AA; 19637 MW; D98A7C95DAB29BD6 CRC64;
Query Match 90.4%; Score 47; DB 1; Length 166;
Best Local Similarity 80.0%; Pred. NO. 0.03;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 VHLGAGISRS 10
DDB 106 VHCWAGINS 115
|||||
|||||
Search completed: September 23, 2004, 14:19:18
Job time : 11 secs

```

Search completed: September 23, 2004, 14:19:18
Job time : 11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

on: September 23, 2004, 14:18:58 ; Search time 42 Seconds
(without alignments)
75.123 Million cell updates/sec

title: US-09-964-277-16

fect score: 52

quence: 1 VHCLAGISRS 10

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

sarched: 1017041 seqs, 315518202 residues 1017041

otal number of hits satisfying chosen parameters:

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match %	Length	ID	Description
1	52	100.0	104	13 Q800X3	Q800X3 gallus gall
2	52	100.0	141	11 Q8R3L7	Q8R3L7 mus musculus
3	52	100.0	362	13 Q803B2	Q803B2 brachydanio
4	52	100.0	368	4 Q8NFJ0	Q8NFJ0 homo sapien
5	52	100.0	369	5 Q44128	Q44128 caenorhabdi
6	52	100.0	378	13 Q91663	Q91663 xenopus lae
7	52	100.0	382	13 Q7T2L9	Q7T2L9 gallus gall
8	52	100.0	382	13 Q7T2L8	Q7T2L8 brachydanio
9	52	100.0	383	13 Q8UW48	Q8UW48 fugu rubrip
10	52	100.0	616	4 Q8NST1	Q8NST1 homo sapien
11	52	100.0	625	4 Q86SS8	Q86SS8 homo sapien
12	52	100.0	652	4 Q81VT8	Q81VT8 homo sapien
13	52	100.0	665	4 Q96N49	Q96N49 homo sapien
14	52	100.0	665	11 Q7TSZ9	Q7TSZ9 mus musculus
15	51	98.1	88	4 P78512	P78512 homo sapien
16	51	98.1	184	4 Q9NRW4	Q9NRW4 homo sapien

17	51	98.1	184	11 Q99N11	Q99N11 mus musculus
18	51	98.1	241	5 Q3VVM4	Q3VVM4 drosophila
19	51	98.1	290	5 Q86P14	Q86P14 drosophila
20	51	98.1	300	11 Q9AG15	Q9AG15 mus musculus
21	51	98.1	354	4 Q8N4A4	Q8N4A4 homo sapien
22	51	98.1	355	11 Q9AG16	Q9AG16 mus musculus
23	51	98.1	411	5 Q95SV1	Q95SV1 drosophila
24	51	98.1	411	5 Q3VVM5	Q3VVM5 drosophila
25	51	98.1	436	11 Q99K22	Q99K22 mus musculus
26	51	98.1	439	5 Q81G35	Q81G35 caenorhabdi
27	51	98.1	452	11 Q8KJ59	Q8KJ59 mus musculus
28	51	98.1	452	11 Q7TNL7	Q7TNL7 mus musculus
29	51	98.1	606	5 Q8ST18	Q8ST18 caenorhabdi
30	51	98.1	622	11 Q99MG5	Q99MG5 mus musculus
31	51	98.1	657	5 Q8ST19	Q8ST19 caenorhabdi
32	51	98.1	660	11 Q920R2	Q920R2 mus musculus
33	51	98.1	677	11 Q99MG6	Q99MG6 mus musculus
34	49	94.2	272	5 Q9XVE7	Q9XVE7 caenorhabdi
35	48	92.3	226	5 Q93592	Q93592 caenorhabdi
36	48	92.3	327	5 Q81QK1	Q81QK1 drosophila
37	48	92.3	327	5 Q81QK0	Q81QK0 drosophila
38	48	92.3	330	3 Q13632	Q13632 schizosacch
39	48	92.3	447	5 Q9VU80	Q9VU80 drosophila
40	47	90.4	168	16 Q89S54	Q89S54 bradyrhizob
41	47	90.4	183	16 Q98KV6	Q98KV6 rhizobium 1
42	47	90.4	212	5 Q9VAB0	Q9VAB0 drosophila
43	46	88.5	142	12 Q55737	Q55737 chilo iride
44	46	88.5	165	12 Q9EMX1	Q9EMX1 ansacta moo
45	46	88.5	169	12 Q98249	Q98249 molluscum c

ALIGNMENTS

RESULT 1

Q800X3 PRELIMINARY; PRT; 104 AA.
 ID Q800X3;
 AC Q800X3;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Dual specificity phosphatase 6 (Fragment).
 GN DUSP6.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Henrique D.M.P., Vieira C.S.L.;
 RT "Cloning of chick dual specificity phosphatase 6";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AY207465; AAC49007.1; -;
 DR GO; GO:0017017; P:MAP kinase phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR008343; MAPK_phosph.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR PRINTS; PR01764; MAPKPHPTASE.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 FT NON_TER 1
 FT NON_TER 104 104
 SQ SEQUENCE 104 AA; 11748 MW; 60563C9B2AE1B753 CRC64;

Query Match 100.0%; Score 52; DB 13; Length 104;

Best Local Similarity 100.0%; Pred. NO. 0.0087;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10

DR	SMART; SM00195; DSPC; 1.
DR	SMART; SM00450; RHOD; 1.
DR	PROSITE; PS0206; RHODANESE_3; 1.
DR	PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
DR	PROSITE; PSS0054; TYR_PHOSPHATASE_DUAL; 1.
SQ	SEQUENCE 362 AA; 40187 MW; 82868A/CBBAB836F6 CRC64;
Query Match 100.0%; Score 52; DB 13; Length 362;	
Best Local Similarity 100.0%; Pred.No. 0.029;	
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 VHCLAGISRS 10
DB	274 VHCLAGISRS 283
RESULT 4	
Q8NFJ0	PRELIMINARY; PRT; 368 AA.
ID	AC Q8NFJ0;
DT	01-OCT-2002 (TREMBLrel. 22, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Dual-specificity phosphatase 7 PYST2-L.
GN	PYST2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NBFI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Levy-Nissenbaum O., Sagi-Assif O., Witz I.P.;
RT	"Complete PYST2-L cDNA";
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
DR	EMBL; AF508727; AAM77606.1; "
DR	GO; GO:0017017; F-MAP kinase phosphatase activity; IEA.
DR	GO; GO:006470; P-protein amino acid dephosphorylation; IEA.
DR	InterPro; IPR000340; DS phosphatase.
DR	InterPro; IPR008343; MAPK_phosph.
DR	InterPro; IPR001763; Rhodanese-like.
DR	InterPro; IPR000387; TYR_phosphatase.
DR	Pfam; PF00782; DSPC; 1.
DR	Pfam; PF00581; Rhodanese; 1.
DR	PRINTS; PR01764; MAPKPHPTASE.
DR	SMART; SM00195; DSPC; 1.
DR	SMART; SM00450; RHOD; 1.
DR	PROSITE; PS0206; RHODANESE_3; 1.
DR	PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
DR	PROSITE; PSS0054; TYR_PHOSPHATASE_DUAL; 1.
SQ	SEQUENCE 368 AA; 40550 MW; 097023C27EBC341C CRC64;
Query Match 100.0%; Score 52; DB 4; Length 368;	
Best Local Similarity 100.0%; Pred.No. 0.03;	
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 VHCLAGISRS 10
DB	278 VHCLAGISRS 287
RESULT 5	
O44128	PRELIMINARY; PRT; 369 AA.
ID	AC O44128;
DT	01-JUN-1998 (TREMBLrel. 06, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Lip-1 protein (corresponding sequence C05B10.1).
GN	C05B10.1 OR Lip-1.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoidea; Chromadorea; Rhabditiida; Rhabditoidea;
OC	Rhabditiidae; Peloderinae; Caenorhabditis.
OX	NBFI_TaxID=6239;

[1] SEQUENCE FROM N.A.
 C STRAIN=Bristol N2;
 K MEDLINE=99069613; PubMed=9851916;
 A Waterston R.;
 T "Genome sequence of the nematode C. elegans: a platform for
 I investigating biology. The C. elegans Sequencing Consortium.";
 L Science 282:2012-2018(1998).
 [2]
 N SEQUENCE FROM N.A.
 P STRAIN=Bristol N2;
 C STRAIN=Bristol N2;
 A Geisel C., Wameley P.;
 T "The sequence of C. elegans cosmid C05B10.";
 L Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 N SEQUENCE FROM N.A.
 P STRAIN=Bristol N2;
 C STRAIN=Bristol N2;
 A Waterston R.;
 L Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 R EMBL; AF036685; AAB88308.2; -;
 R F1R; T32494; T32494.
 R HSP; Q16828; IMKP.
 R WormPep; C05B10.1; C031151.
 R GO; GO:0017017; F:MAP kinase phosphatase activity; IEA.
 R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 R InterPro; IPR000340; DS phosphatase.
 R InterPro; IPR008343; MAPK phosph.
 R InterPro; IPR000387; TYR_phosphatase.
 R Pfam; PF00782; DSPC; 1.
 R PRINTS; PR01764; MAPKPHPTASE.
 R SMART; SM00195; DSPC; 1.
 R PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 R PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
 Q SEQUENCE 369 AA; 41586 MW; 5A13DEA9C5198A17 CRC64;
 Query Match 100.0%; Score 52; DB 5; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 VHCLAGISRS 10
 |||||
 b 269 VHCLAGISRS 278

RESULT 6
 D Q91663 PRELIMINARY; PRT; 378 AA.
 C Q91663;
 T 01-NOV-1996 (TrEMBLrel. 01, Created)
 T 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 E Dual specificity protein phosphatase ? (EC 3.1.3.48) (EC 3.1.3.16)
 S (MAP kinase phosphatase X17C).
 S Xenopus laevis (African clawed frog).
 C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 C Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 C Xenopodinae; Xenopus.
 X NCBI_TaxID=8355;
 X NCBI_TaxID=8355;
 [1]
 N SEQUENCE FROM N.A.
 P TISSUE=EMBRYO;
 C MEDLINE=95319535; PubMed=7541116;
 X Umbhauer M., Marshall C.J., Mason C.S., Old R.W., Smith J.C.;
 T "Mesoderm induction in Xenopus caused by activation of MAP kinase.";
 L Nature 376:58-62(1995).
 L Nature 376:58-62(1995).
 C -1- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
 PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
 SIMILARITY).
 C -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
 TYROSINE + PHOSPHATE.
 C -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 C -1- TISSUE SPECIFICITY: LOCALISED IN THE BRANCHIAL ARCH REGION AND
 TAIL TIP.

CC -1- INDUCTION: BY RETINOIC ACID.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS THE CDC25 HOMOLOGY DOMAINS 2 A AND B (CH2
 CC DOMAINS A AND B).
 DR EMBL; U43223; AAA85240.1; -;
 DR HSP; Q16828; IMKP.
 DR GO; GO:0004723; P:calcium-dependent protein serine/threonine . . .; IEA.
 DR GO; GO:0008420; F:CTD phosphatase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004724; F:magnesium-dependent protein serine/threonin. . .; IEA.
 DR GO; GO:0017017; F:MAP kinase phosphatase activity; IEA.
 DR GO; GO:0017018; F:myosin phosphatase activity; IEA.
 DR GO; GO:0000158; F:protein phosphatase type 2A activity; IEA.
 DR GO; GO:0003035; F:protein phosphatase type 2B activity; IEA.
 DR GO; GO:0015071; F:protein phosphatase type 2C activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000340; DS phosphatase.
 DR InterPro; IPR008343; MAPK_phosph.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR PRINTS; PR01764; MAPKPHPTASE.
 DR SMART; SM00195; DSPC; 1.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS00056; RHODANES 3; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase.
 FT DOMAIN 34 49 CH2 A DOMAIN.
 FT DOMAIN 126 141 CH2 B DOMAIN.
 FT DOMAIN 152 158 POLY-SER.
 FT DOMAIN 205 378 CATALYTIC.
 FT ACT_SITE 290 290 BY SIMILARITY.
 SQ SEQUENCE 378 AA; 42036 MW; F274D4CAE960B783 CRC64;
 Query Match 100.0%; Score 52; DB 13; Length 378;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHCLAGISRS 10
 |||||
 DB 289 VHCLAGISRS 297

RESULT 7
 Q7T2L9
 ID Q7T2L9 PRELIMINARY; PRT; 382 AA.
 AC Q7T2L9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MAP kinase phosphatase 3.
 GN MKP3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 X NCBI_TaxID=9031;
 X NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22660508; PubMed=12766772;
 RA Kawakami Y., Rodriguez-Leon J., Koth C.M., Buscher D., Itoh T.,
 RA Raya A., Ng J.K., Rodriguez Esteban C., Takahashi S., Henrique D.,
 RA Schwarz M.-F., Asahara H., Izpisua Belmonte J.C.;
 RT "MKP3 mediates the cellular response to FGF8 signalling in the
 vertebrate limb.";
 RL Nat. Cell Biol. 5:513-519(2003).
 DR EMBL; AY278202; AAP69999.1; -;
 KW Kinase.
 SQ SEQUENCE 382 AA; 42528 MW; 9BCAD902098A93B8 CRC64;

Query Match 100.0%; Score 52; DB 13; Length 382;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 DB 292 VHCLAGISRS 301
 |||||

RESULT 8
 Q7T2L8 PRELIMINARY; PRT; 382 AA.
 AC Q7T2L8
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE MAP kinase phosphatase 3.
 GN MKP3.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=22660508; PubMed=12766772;
 RA Kawakami Y., Rodriguez-Leon J., Koth C.M., Buscher D., Itoh T.,
 RA Rava A., Ng J.K., Rodriguez Esteban C., Takahashi S., Henrique D.,
 RA Schwarz M.-P., Asahara H., Izpisua Belmonte J.C.;
 RT "MKP3 mediates the cellular response to FGF8 signalling in the
 RT vertebrate limb.";
 RL Nat. Cell Biol. 5:513-519(2003).
 DR EMBL: AV278203; AAP70000.1; -.
 KW Kinase.
 SQ SEQUENCE 382 AA; 42860 MW; 50E773D7CE797BB1 CRC64;

Query Match 100.0%; Score 52; DB 13; Length 382;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 DB 290 VHCLAGISRS 299
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RESULT 9
 Q8UW48 PRELIMINARY; PRT; 383 AA.
 AC Q8UW48
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Dual specificity phosphatase 6, isoform a.
 GN DUSP6.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontoidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 SEQUENCE FROM N.A.
 RP Ayele K., Beckstrom-Sternberg S.M., Benjamin B., Blakesley R.W.,
 RA Bouffard G.G., Brinkley C., Brooks S., Dietrich N.L., Granite S.,
 RA Guan X., Gupta J., Ho S.-L., Idol J.R., Karlins E., Lee-Lin S.-Q.,
 RA Legaspi R., Lim M., Madero Q.L., Maduro V.B., Masiello C.,
 RA Masrjian S.D., McCloskey J.C., McDowell J., Pearson R., Prasad A.,
 RA Shevchenko Y., Snyder B., Stantripop S., Thomas J.W., Thomas P.J.,
 RA Tjongson E.S., Touchman J.W., Taurgeon C., Vogt J.L., Walker M.A.,
 RA Wetherby K.D., Zhang L.-H., Green E.D.;
 RT "NISC Comparative Sequencing Initiative."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC090119; AAL40358.1; -.

DR HSSP; Q16928; 1MKP.
 DR GO; GO:0017017; F:MAP kinase phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000340; DS phosphatase.
 DR InterPro; IPR008343; MAPK phosph.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR000387; TYR phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR Pfam; PF00581; Rhodanese; 1.
 DR PRINTS; PR01764; MAPKPHPTASE.
 DR SMART; SM00195; DSPC; 1.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS50206; RHODANESE 3; 1.
 DR PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
 DR PROSITE; PS50054; TYR PHOSPHATASE_DUAL; 1.
 SQ SEQUENCE 383 AA; 42831 MW; 0804F64E9C8E49B8 CRC64;

Query Match 100.0%; Score 52; DB 13; Length 383;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 DB 291 VHCLAGISRS 300
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RESULT 10
 Q8N5T1 PRELIMINARY; PRT; 616 AA.
 AC Q8N5T1
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 RP TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC031643; AAH31643.1; -.
 DR GO; GO:0017017; F:MAP kinase phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000340; DS phosphatase.
 DR InterPro; IPR008343; MAPK phosph.
 DR InterPro; IPR000387; TYR phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR PRINTS; PR01764; MAPKPHPTASE.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
 DR PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
 DR PROSITE; PS50054; TYR PHOSPHATASE_DUAL; 1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 616 AA; 67636 MW; 2CB0B14482F2AD72 CRC64;

Query Match 100.0%; Score 52; DB 4; Length 616;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
 DB 193 VHCLAGISRS 202
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RESULT 11
 Q86SS8 PRELIMINARY; PRT; 625 AA.
 ID Q86SS8
 AC Q86SS8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)

01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Similar to dual specificity phosphatase 8.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Brain, and Astrocytoma;
 Strausberg R.;
 Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 EMBL; BC045110; AAH45110.1; -
 GO; GO:0017017; P:MAP kinase phosphatase activity; IEA.
 GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 InterPro; IPR000340; DS phosphatase.
 InterPro; IPR008343; MAPK phosph.
 InterPro; IPR002965; P rich exten.
 InterPro; IPR001763; Rhodanese-like.
 InterPro; IPR000387; TYR phosphatase.
 Pfam; PF00782; DSPC; 1.
 PRINTS; PRO1764; MAPKPHPTASE.
 PRINTS; PRO1217; PRICHEXTENSN.
 SMART; SM00195; DSPC; 1.
 SMART; SM00450; RHOD; 1.
 PROSITE; PS50206; RHODANES_3; 1.
 PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 SEQUENCE 625 AA; 65826 MW; C7C808407B724FFC CRC64;
 Query Match 100.0%; Score 52; DB 4; Length 625;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 VHCLAGISRS 10
 |||||
 244 VHCLAGISRS 253

SO SEQUENCE 662 AA; 72818 MW; 350534EF0652B98F CRC64;
 Query Match 100.0%; Score 52; DB 4; Length 662;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 VHCLAGISRS 10
 |||||
 242 VHCLAGISRS 251

RESULT 13
 Q96N49 PRELIMINARY; PRT; 665 AA.
 AC Q96N49;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ31411.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 Otsuki T., Sato H., Wakamatsu A., Iehli S., Yamamoto J., Isono Y.,
 Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
 Isogai T.;
 "NEO human cDNA sequencing project";
 Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 EMBL; AK055973; BAB71060.1; -
 DR HSP; Q16828; 1MKP.
 DR GO; GO:0016787; P:hydrolase activity; IEA.
 DR GO; GO:0017017; P:MAP kinase phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000340; DS phosphatase.
 DR InterPro; IPR008343; MAPK phosph.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR000387; TYR phosphatase.
 Pfam; PF00782; DSPC; 1.
 Pfam; PF00581; Rhodanese; 1.
 PRINTS; PRO1764; MAPKPHPTASE.
 SMART; SM00195; DSPC; 1.
 SMART; SM00450; RHOD; 1.
 PROSITE; PS50206; RHODANES_3; 1.
 PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hypothetical protein; Hydrolase.
 SQ SEQUENCE 665 AA; 73058 MW; 1EAE0DF08460DFF CRC64;
 Query Match 100.0%; Score 52; DB 4; Length 665;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 VHCLAGISRS 10
 |||||
 242 VHCLAGISRS 251

RESULT 14
 Q7TS29 PRELIMINARY; PRT; 665 AA.
 AC Q7TS29;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Dusp8 protein.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MFLINE=22388257; PubMed12477932;
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC052705; AAHS2705.1; -;
 SQ SEQUENCE 665 AA; 69021 MW; 9166E36A8835249F CRC64;

Query Match 100.0%; Score 52; DB 11; Length 665;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VHCLAGISRS 10
 DB 244 VHCLAGISRS 253

RESULT 15
 P78512
 ID P78512 PRELIMINARY; PRT; 68 AA.
 AC P78512;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Dual specificity protein phosphatase homolog hMKP-R (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Dayton M.D.;
 RT "Multiple phosphotyrosine phosphatase mRNAs are expressed in the human
 RT lung fibroblast cell line WI-38.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U87167; AA847559.1; -;
 DR HSSP; Q16828; IMKP.
 DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphatase.; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000340; DS phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.

FT NON_TER 1
 FT NON_TER 68
 SQ SEQUENCE 68 AA; 7592 MW; 3AAACCB6D0D3394A CRC64;
 Query Match 98.1%; Score 51; DB 4; Length 68;
 Best Local Similarity 90.0%; Pred. No. 0.0092;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VHCLAGISRS 10
 DB 21 VHCLAGISRS 30

Search completed: September 23, 2004, 14:21:10
 Job time : 48 secs

Sequence 17, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 13, Appl
Sequence 4, Appl
Sequence 7, Appl
Sequence 5, Appl
Sequence 806, App
Sequence 806, App
Sequence 806, App
Sequence 806, App
Sequence 806, App
Sequence 7, Appl

28 46 88.5 168 4 US-09-619-380-17
29 46 88.5 169 4 US-09-544-716-16
30 46 88.5 169 4 US-09-544-716-17
31 46 88.5 169 4 US-09-557-921-17
32 46 88.5 169 4 US-09-557-921-18
33 46 88.5 169 4 US-09-564-357-19
34 46 88.5 169 4 US-09-564-357-20
35 46 88.5 169 4 US-09-619-380-18
36 46 88.5 169 4 US-09-619-380-19
37 46 88.5 173 4 US-09-704-139-4
38 46 88.5 173 4 US-09-816-494-7
39 46 88.5 198 3 US-09-045-973-5
40 46 88.5 302 4 US-09-702-705-806
41 46 88.5 302 4 US-09-736-457-806
42 46 88.5 302 4 US-09-614-124B-806
43 46 88.5 302 4 US-09-671-325-806
44 46 88.5 302 4 US-09-589-184-806
45 46 88.5 313 2 US-08-990-379-7

ALIGNMENTS

RESULT 1
US-09-371-671B-9
; Sequence 9, Application US/09371671B
; Patent No. 6548743
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; APPLICANT: Chiu, Wan-Ling
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
; FILE REFERENCE: 00786/370002
; CURRENT APPLICATION NUMBER: US/09/371,671B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/155,934
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/095,938
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Rat rattus
US-09-371-671B-9

Query Match 100.0%; Score 52; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.007; 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 1 VHCLAGISRS 10
DB 34 VHCLAGISRS 43

RESULT 2
US-09-544-716-13
; Sequence 13, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens

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on on: September 23, 2004, 14:19:05 ; Search time 18 Seconds
(without alignments)
28.681 Million cell updates/sec

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Maximum Match 100%

Listing first 45 summaries

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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/1aa/backfills1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	87	4	US-09-371-671B-9
2	52	100.0	168	4	US-09-544-716-13
3	52	100.0	168	4	US-09-557-921-13
4	52	100.0	168	4	US-09-564-357-16
5	52	100.0	168	4	US-09-619-380-15
6	52	100.0	170	4	US-09-544-716-12
7	52	100.0	170	4	US-09-544-716-14
8	52	100.0	170	4	US-09-557-921-12
9	52	100.0	170	4	US-09-557-921-15
10	52	100.0	170	4	US-09-564-357-15
11	52	100.0	170	4	US-09-564-357-17
12	52	100.0	170	4	US-09-619-380-14
13	52	100.0	170	4	US-09-619-380-16
14	52	100.0	665	4	US-09-816-494-2
15	48	92.3	226	3	US-09-045-973-8
16	46	88.5	23	4	US-09-544-716-5
17	46	88.5	23	4	US-09-564-357-6
18	46	88.5	24	4	US-09-619-380-4
19	46	88.5	45	2	US-08-530-290-21
20	46	88.5	72	2	US-08-530-290-19
21	46	88.5	87	4	US-09-371-671B-7
22	46	88.5	87	4	US-09-371-671B-8
23	46	88.5	117	1	US-07-988-273-4
24	46	88.5	117	5	PCT-US93-12019-4
25	46	88.5	168	4	US-09-544-716-15
26	46	88.5	168	4	US-09-557-921-16
27	46	88.5	168	4	US-09-564-357-18

US-09-544-716-13

Query Match 100.0%; Score 52; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | |
Db 108 VHCLAGISRS 117

RESULT 3

US-09-557-921-13
; Sequence 13, Application US/09557921
; Patent No. 6551810

; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.

; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921

; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13

; LENGTH: 168
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-557-921-13

Query Match 100.0%; Score 52; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | |
Db 108 VHCLAGISRS 117

RESULT 4

US-09-564-357-16
; Sequence 16, Application US/09564357
; Patent No. 6645753

; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.

; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357

; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16

; LENGTH: 168
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-564-357-16

Query Match 100.0%; Score 52; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | |
Db 108 VHCLAGISRS 117

RESULT 5

US-09-619-380-15
; Sequence 15, Application US/09619380
; Patent No. 6649391

; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.

; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380

; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15

; LENGTH: 168
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-619-380-15

RESULT 6

US-09-544-716-12
; Sequence 12, Application US/09544716
; Patent No. 6492157

; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.

; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716

; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12

; LENGTH: 170
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-544-716-12

Query Match 100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | |
Db 110 VHCLAGISRS 119

RESULT 7

US-09-544-716-14
; Sequence 14, Application US/09544716
; Patent No. 6492157

; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.

; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716

; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14

; LENGTH: 170
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-544-716-14

Query Match 100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-15

Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
        |||||
Db       110 VHCLAGISRS 119
        |||||

RESULT 11
US-09-564-357-17
; Sequence 17, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357
; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-17

Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
        |||||
Db       110 VHCLAGISRS 119
        |||||

RESULT 12
US-09-619-380-14
; Sequence 14, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-619-380-14

Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
        |||||
Db       110 VHCLAGISRS 119
        |||||

RESULT 13
US-09-619-380-14
; Sequence 15, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357
; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22
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US-09-619-380-16

; Sequence 16, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-619-380-16

Query Match 100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
Db 110 VHCLAGISRS 119
|||||

RESULT 14

US-09-816-494-2
; Sequence 2, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-816-494-2

Query Match 100.0%; Score 52; DB 4; Length 665;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
Db 242 VHCLAGISRS 251
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RESULT 15

US-09-045-973-8
; Sequence 8, Application US/09045973
; Patent No. 6165767
; GENERAL INFORMATION:

; APPLICANT: Lal, Preeti
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: PROTEIN PHOSPHATASE RELATED MOLECULES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,973
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0491 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1495338
US-09-045-973-8

Query Match 92.3%; Score 48; DB 3; Length 226;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
Db 96 VHCVAGVRS 105
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Job time : 19 secs

4 protein - protein search, using sw model
on on: September 23, 2004, 14:21:14 ; Search time 129 Seconds
(without alignments)
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itle: US-09-964-277-16
rfect score: 52
equence: 1 VHCLAGISRS 10

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Maximum Match 100%
Listing first 45 summaries

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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB	ID	Description
1	52	100.0	10	9	US-09-964-277-16	Sequence 16, Appl
2	52	100.0	41	9	US-09-964-277-13	Sequence 13, Appl
3	52	100.0	155	9	US-09-964-277-6	Sequence 6, Appli
4	52	100.0	155	9	US-09-964-277-7	Sequence 7, Appli
5	52	100.0	155	9	US-09-955-732-6	Sequence 6, Appli
6	52	100.0	156	9	US-09-964-277-3	Sequence 3, Appli
7	52	100.0	156	9	US-09-964-277-4	Sequence 4, Appli
8	52	100.0	156	9	US-09-955-732-3	Sequence 4, Appli
9	52	100.0	156	9	US-09-955-732-4	Sequence 4, Appli
10	52	100.0	167	14	US-10-346-356-13	Sequence 13, Appl
11	52	100.0	168	9	US-09-775-925-24	Sequence 24, Appl
12	52	100.0	168	9	US-09-847-519A-9	Sequence 9, Appli
13	52	100.0	168	12	US-10-655-073-15	Sequence 15, Appl
14	52	100.0	168	14	US-10-314-058-13	Sequence 13, Appl
15	52	100.0	168	14	US-10-405-808-15	Sequence 15, Appl

16 52 100.0 169 14 US-10-346-356-12 Sequence 12, Appl
17 52 100.0 169 14 US-10-346-356-15 Sequence 15, Appl
18 52 100.0 170 9 US-09-775-925-23 Sequence 23, Appl
19 52 100.0 170 9 US-09-775-925-26 Sequence 26, Appl
20 52 100.0 170 9 US-09-847-519A-8 Sequence 8, Appli
21 52 100.0 170 9 US-09-847-519A-11 Sequence 11, Appl
22 52 100.0 170 12 US-10-655-073-14 Sequence 14, Appl
23 52 100.0 170 12 US-10-655-073-16 Sequence 16, Appl
24 52 100.0 170 14 US-10-314-058-12 Sequence 12, Appl
25 52 100.0 170 14 US-10-314-058-14 Sequence 14, Appl
26 52 100.0 170 14 US-10-405-808-14 Sequence 14, Appl
27 52 100.0 170 14 US-10-405-808-16 Sequence 16, Appl
28 52 100.0 189 9 US-09-925-299-842 Sequence 842, App
29 52 100.0 189 10 US-09-925-299-842 Sequence 33, Appl
30 52 100.0 322 12 US-10-060-065-33 Sequence 54, Appl
31 52 100.0 322 14 US-10-059-585-54 Sequence 2, Appli
32 52 100.0 381 12 US-10-184-832-2 Sequence 2, Appli
33 52 100.0 419 16 US-10-472-380-2 Sequence 702, App
34 52 100.0 501 12 US-10-072-012-702 Sequence 21, Appl
35 52 100.0 517 9 US-09-964-277-21 Sequence 699, App
36 52 100.0 625 12 US-10-072-012-599 Sequence 258, App
37 52 100.0 662 12 US-10-072-012-258 Sequence 700, App
38 52 100.0 663 12 US-10-072-012-700 Sequence 2, Appli
39 52 100.0 665 9 US-09-816-494-2 Sequence 2, Appli
40 52 100.0 665 9 US-09-964-277-2 Sequence 680, App
41 52 100.0 665 12 US-10-072-012-680 Sequence 681, App
42 52 100.0 665 12 US-10-072-012-681 Sequence 14, Appl
43 52 100.0 665 12 US-10-168-506-14 Sequence 7, Appli
44 52 100.0 665 12 US-10-343-357-7 Sequence 2312, Ap
45 52 100.0 665 15 US-10-094-749-2312

ALIGNMENTS

RESULT 1
US-09-964-277-16
; Sequence 16, Application US/09964277
; Patent No. US2002013170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-16

Query Match 100.0%; Score 52; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
Db 1 VHCLAGISRS 10
|||||

RESULT 2
US-09-964-277-13
; Sequence 13, Application US/09964277
; Patent No. US2002013170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277

; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-13

Query Match 100.0%; Score 52; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
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Db 11 VHCLAGISRS 20

RESULT 3
US-09-964-277-6
; Sequence 6, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-6

Query Match 100.0%; Score 52; DB 9; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
| | | | | | | | | |
Db 96 VHCLAGISRS 105

RESULT 4
US-09-964-277-7
; Sequence 7, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-7

Query Match 100.0%; Score 52; DB 9; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
| | | | | | | | | |
Db 96 VHCLAGISRS 105

RESULT 5
US-09-955-732-6
; Sequence 6, Application US/09955732
; Publication No. US20020182203A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732-6

Query Match 100.0%; Score 52; DB 9; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
| | | | | | | | | |
Db 96 VHCLAGISRS 105

RESULT 6
US-09-964-277-3
; Sequence 3, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-3

Query Match 100.0%; Score 52; DB 9; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCLAGISRS 10
| | | | | | | | | |
Db 97 VHCLAGISRS 106

RESULT 7
US-09-964-277-4
; Sequence 4, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 156

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ORGANISM: Homo sapiens
-09-964-277-4

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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 VHCLAGISRS 10
      |||||
      97 VHCLAGISRS 106

RESULT 8
-09-955-732-3
Sequence 3, Application US/09955732
Publication No. US20020182203A1
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.433
CURRENT APPLICATION NUMBER: US/09/955,732
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 156
TYPE: PRT
ORGANISM: Homo sapiens
-09-955-732-3

Query Match      100.0%; Score 52; DB 9; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 VHCLAGISRS 10
      |||||
      97 VHCLAGISRS 106

RESULT 9
-09-955-732-4
Sequence 4, Application US/09955732
Publication No. US20020182203A1
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.433
CURRENT APPLICATION NUMBER: US/09/955,732
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 156
TYPE: PRT
ORGANISM: Homo sapiens
-09-955-732-4

Query Match      100.0%; Score 52; DB 9; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 VHCLAGISRS 10
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      97 VHCLAGISRS 106

RESULT 10
-10-346-356-13
Sequence 13, Application US/10346356
Publication No. US20030138931A1
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.416C1
CURRENT APPLICATION NUMBER: US/10/346,356
CURRENT FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 167
TYPE: PRT
ORGANISM: Homo sapiens
-10-346-356-13

Query Match      100.0%; Score 52; DB 14; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 VHCLAGISRS 10
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      108 VHCLAGISRS 117

RESULT 11
US-09-775-925-24
Sequence 24, Application US/09775925
Patent No. US20010049358A1
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
FILE REFERENCE: 200125.420
CURRENT APPLICATION NUMBER: US/09/775,925
CURRENT FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 168
TYPE: PRT
ORGANISM: Homo sapiens
US-09-775-925-24

Query Match      100.0%; Score 52; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 VHCLAGISRS 10
      |||||
      108 VHCLAGISRS 117

RESULT 12
US-09-847-519A-9
Sequence 9, Application US/09847519A
Patent No. US20020102693A1
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.422
CURRENT APPLICATION NUMBER: US/09/847,519A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 168
TYPE: PRT
ORGANISM: Homo sapiens
US-09-847-519A-9

Query Match      100.0%; Score 52; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VHCLAGISRS 10
    |||||
Db 108 VHCLAGISRS 117

RESULT 13
US-10-655-073-15
; Sequence 15, Application US/10655073
; Publication No. US20040043411A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418C1
; CURRENT APPLICATION NUMBER: US/10/655,073
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-655-073-15

Query Match 100.0%; Score 52; DB 14; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
    |||||
Db 108 VHCLAGISRS 117

Search completed: September 23, 2004, 14:32:40
Job time : 139 secs
```

```
Query Match 100.0%; Score 52; DB 12; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VHCLAGISRS 10
    |||||
Db 108 VHCLAGISRS 117
```

```
RESULT 14
US-10-314-058-13
; Sequence 13, Application US/10314058
; Publication No. US20030119045A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415C1
; CURRENT APPLICATION NUMBER: US/10/314,058
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-058-13
```

```
Query Match 100.0%; Score 52; DB 14; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VHCLAGISRS 10
    |||||
Db 108 VHCLAGISRS 117
```

```
RESULT 15
US-10-405-808-15
; Sequence 15, Application US/10405808
; Publication No. US20030175829A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-4 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.410C1
; CURRENT APPLICATION NUMBER: US/10/405,808
```